

# Fig.1.

Sequence ID 1

```
1  TCGG AGG GGT GCA AGG AGT TCT TCA GGC GGA GTG TAA CCA AAA ATG
   ACGC TCC CCA CGT TCC TCA AGA AGT CCG CCT CAC ATT GGT TTT TAC

46 CAG TGT ACA TAT GCA AAT TCG GCC ATG CTT GCG AAA TGG ATA TGT
   GTC ACA TGT ATA CGT TTA AGC CGG TAC GAA CGC TTT ACC TAT ACA

91 ATA TGC GGA GAA AAT GCC AAG AGT A
   TAT ACG CCT CTT TTA CGG TTC TCA T
```

Fig.2.

Sequence ID 2

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   | TCC | ACT | GGT | GTT | TTC | ACC | ACC | ACA | GAA | AAG | GCC | TCT | GCT | CAT | TTA |
|     | AGG | TGA | CCA | CAA | AAG | TGG | TGG | TGT | CTT | TTC | CGG | AGA | CGA | GTA | AAT |
| 46  | GAG | GGT | GGT | GCT | AAG | AAG | GTC | ATC | ATC | TCC | TGC | TGC | CCA | GCG | CTG |
|     | CTC | CCA | CCA | CGA | TTC | TTC | CAG | TAG | TAG | AGG | ACG | ACG | GGT | CGC | GAC |
| 91  | ACC | CAT | GTT | CGT | CGT | TGG | TGT | CAA | CCT | TGA | AGC | AGT | ATG | ACC | CCT |
|     | TGG | GTA | CAA | GCA | GCA | ACC | ACA | GTT | GGA | ACT | TCG | TCA | TAC | TGG | GGA |
| 136 | CTT | ACA | AGG | TCA | TCT | CCA | ACG | CCT | CCT | GCA | CAA | CCA | ACT | GCC | TCG |
|     | GAA | TGT | TCC | TCC | AGT | AGA | GGT | GGA | GGA | CGT | GTT | GGT | TGA | CGG | AGC |
| 181 | CTC | CTC | TCG | CTA | AGG | TCA | TCC | ATG | ACA | ACT | TCG | AGA | TCA | TTG | AAG |
|     | GAG | GAG | AGC | GAT | TCC | AGT | AGG | TAC | TGT | TGA | AGC | TCT | AGT | AAC | TTC |
| 226 | GTC | TGA | TGA | CCA | CTG | TAC | ACG | CCA | CCA | CTG | CCA | CCC | AGA | AGA | CAG |
|     | CAG | ACT | ACT | GGT | GAC | ATG | TGC | GGT | GGT | GAC | GGT | GGG | TCT | TCT | GTC |
| 271 | TGG | ATG | GAC | CCT | CTG | GTA | AAC | TGT | GGC | GTG | ATG | GCC | GTG | GTG | CTC |
|     | ACC | TAC | CTG | GGA | GAC | CAT | TTG | ACA | CCG | CAC | TAC | CGG | CAC | CAC | GAG |
| 316 | AGC | AGA | ATA | TCA | TTC | CCG | CGG | AAT | TCC | CCA | GCC | GCA | GCT | AGC | TAA |
|     | TCG | TCT | TAT | AGT | AAG | GGC | GCC | TTA | AGG | GGT | CGG | CGT | CGA | TCG | ATT |

Fig.2 i.

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361 CCT GCA GCA GAC ACA ACC CCT ACC TTC CAT GCC GTT ACC AAT GCC
    GGA CGT CGT CTG TGT TGG GGA TGG AAG GTA CGG CAA TGG TTA CGG

406 ACC GAC AAC ACC CAA ATC AGA AAA CGA GTC AAT GTC ATC AGG TCG
    TGG CTG TTG TGG GTT TAG TCT TTT GCT CAG TTA CAG TAG TCC AGC

451 TGA GGA ACT GTC TCC AGC TTC GAG TGT AAA CGG CTG CAG CAC AGA
    ACT CCT TGA CAG AGG TCG AAG CTC ACA TTT GCC GAC GTC GTG TCT

496 TGG CGA GGC GAG GCG GCA GAA AGG CCC AGC GCC GAG GCA GCA
    ACC GCT CCG CTC CGC CGT CTT CTT TCC GGG TCG CGG CTC CGT CGT

541 AGA AGA GCT ATG TCT TGT CTG CGG CGA CAG AGC CTC CGG ATA TCA
    TCT TCT CGA TAC AGA ACA GAC GCC GCT GTC TCG GAG GCC TAT AGT

586 CTA CAA CGC GCT CAC ATG TGA AGG GTG TAA AGG TTT CTT CAG GCG
    GAT GTT GCG CGA GTG TAC ACT TCC CAC ATT TCC AAA GAA GTC CGC

631 GAG TGT AAC CAA AAA TGC AGT GTA CAT ATG CAA ATT CGG CCA TGC
    CTC ACA TTG GTT TTT ACG TCA CAT GTA TAC GTT TAA GCC GGT ACG

676 TTG CGA AAT GGA TAT CTA TAT GCG GAG AAA ATG TCA GGA GTG TCG
    AAC GCT TTA CCT ATA GAT ATA CGC CTC TTT TAC AGT CCT CAC AGC

721 GTT GAA GAA ATG TCT TGC GGT GGG CAT GAG GCC CGA GTG CGT GGT
    CAA CTT CTT TAC AGA ACG CCA CCC GTA CTC CGG GCT CAC GCA CCA

766 GCC GGA GAA CCA GTG TGC AAT GAA ACG GAA AGA GAA AAA GGC GCA
    CGG CCT CTT GGT CAC ACG TTA CTT TGC CTT TCT CTT TTT CCG CGT

```

Fig.2 ii.

811 GAG GGA AAA AGA CAA ATT GCC CGT CAG TAC GAC GAC AGT AGA CGA  
CTC CCT TTT TCT TCT TAA CGG GCA GTC ATG CTG CTG TCA TCT GCT

856 TCA CAT GCC TCC CAT CAT GCA ATG TGA CCC TCC GCC CCC AGA GGC  
AGT GTA CGG AGG GTA GTA CGT TAC ACT GGG AGG CGG GGG TCT CCG

901 CGC TAG AAT TCT GGA ATG TGT GCA GCA CGA GGT GGT GCC ACG ATT  
GCG ATC TTA AGA CCT TAC ACA CGT CGT GCT CCA CGG TGC TAA

946 CCT GAA TGA GAA GCT AAT GGA ACA GAA CAG ATT GAA GAA CGT GCC  
GGA CTT ACT CTT CGA TTA CCT TGT CTT GTC TAA CTT CTT GCA CGG

991 CCC CCT CAC TGC CAA TCA GAA GTC GTT GAT CGC AAG GCT CGT GTG  
GGG GGA GTG ACG GTT AGT CTT CAG CAA CTA GCG TTC CGA GCA CAC

1036 GTA CCA GGA AGG CTA TGA ACA ACC TTC CGA GGA AGA CCT GAA GAG  
CAT GGT CCT TCC GAT ACT TGT TGG AAG GCT CCT TCT GGA CTT CTC

1081 GGT TAC ACA GTC GGA CGA GGA CGA AGA CTC GGA TAT GCC GTT  
CCA ATG TGT CAG CCT GCT GCT CCT GCT GAG CCT ATA CGG CAA

1126 CCG TCA GAT TAC CGA GAT GAC GAT TCT CAC AGT GCA GCT CAT CGT  
GGC AGT CTA ATG GCT CTA CTG CTA AGA GTG TCA CGT CGA GTA GCA

1171 AGA ATT CGC TAA GGG CCT CCC GGG CTT CGC CAA GAT CTC GCA GTC  
TCT TAA GCG ATT CCC GGA GGG CCC GAA GCG GTT CTA GAG CGT CAG

1216 GGA CCA GAT CAC GTT ATT AAA GGC GTG CTC AAG TGA GGT GAT GAT  
CCT GGT CTA GTG CAA TAA TTT CCG CAC GAG TTC ACT CCA CTA CTA

1261 GCT CCG AGT GGC TCG GCG GTA TGA CGC GGC CAC CGA CAG CGT ACT  
CGA GGC TCA CCG AGC CGC CAT ACT GCG CCG GTG GCT GTC GCA TGA

Fig.2 iii.

1306 GTT CGC GAA CAA CCA GGC GTA CAC TCG CGA CAA CTA CCG CAA GGC  
CAA GCG CTT GTT GGT CCG CAT GTG AGC GCT GTT GAT GGC GTT CCG

1351 AGG CAT GGC GTA CGT CAT CGA GGA CCT GCT GCA CTT CTG TCG GTG  
TCC GTA CCG CAT GCA GTA GCT CCT GGA CGA CGT GAA GAC AGC CAC

1396 CAT GTA CTC CAT CAT GAT GAT GGA TAA CGT GCA TTA TGC GCT GCT TAC  
GTA CAT GAG GTA CTA CTA CTT ATT GCA CGT AAT ACG CGA CGA ATG

1441 AGC CAT TGT CAT CTT CTC AGA CCG GCC CGG GCT TGA GCA ACC CCT  
TCG GTA ACA GTA GAA GAG TCT GGC CGG GCC CGA ACT CGT TGG GGA

1486 GTT GGT GGA GGA CAT CCA GAG ATA TTA CCT GAA CAC GCT ACG GGT  
CAA CCA CCT CCT GTA GGT CTC TAT AAT GGA CTT GTG CGA TGC CCA

1531 GTA CAT CCT GAA CCA GAA CAG CGC GTC GCC CGG GCT CGT CAT  
CAT GTA GGA CTT GGT CTT GTC GCG CAG CGG GGC GCC GCG GCA GTA

1576 CTT CGG CGA GAT CCT GGG CAT ACT GAC GGA GAT CCG CAC GCT GGG  
GAA GCC GCT CTA GGA CCC GTA TGA CTG CCT CTA GGC GTG CGA CCC

1621 CAT GCA GAA CTC CAA CAT GTG CAT CTC CCT CAA GCT GAA GAA CAG  
GTA CGT CTT GAG GTT GTA CAC GTA GAG GGA GTT CGA CTT CTT GTC

1666 GAA GCT GCC GCC GTT CCT CGA GGA GAT CTG GGA CGT GGC GGA CGT  
CTT CGA CCG CGG CAA GGA GCT CCT CTA GAC CCT GCA CCG CCT GCA

1711 GGC GAC GAC GGC GAC GCC GGT GGC GGC GGA GGC GCC GGC TCT  
CCG CTG CTG CCG CTG CCG CCA CCG CCG CCT CCG CCG CGG CGG AGA

Fig.2 iv.

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1756 AGC CCC CGC CCC GCC CGC CGC GCC GCC CGC CAC CGT CTA GCG CGC
TCG GGG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG
1801 CTC AGG AGA GAA CGC TCA TAG ACT GGC TAG TTT TAG TGA AGT GCA
GAG TCC TCT CTT GCG AGT ATC TGA CCG ATC AAA ATC ACT TCA CGT
1846 CGG ACA CTG ACG TCG TCG ACG TGA TCA ACC TAT TTA TAA GGA CTG CGA
GCC TGT GAC TGC AGC TGC ACT AGT TGG ATA AAT ATT CCT GAC GCT
1891 ATT TTA CCA CTT AAG AGG GCA CAC CCG TAC CCG ATT TCG TAC GG
TAA AAT GGT GAA TTC TCC CGT GTG GGC ATG GGC TAA AGC ATG CC
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Total number of bases is: 1934.

## Fig.3.

The sequence shown below is that of pSK16.1

Sequence ID3

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   | CGC | TGG | TAT | AAC | AAC | GGA | CCA | TTC | CAG | ACG | CTG | CGA | ATG | CTC | GAG |
|     | GCG | ACC | ATA | TTG | TTG | CCT | GGT | AAG | GTC | TGC | GAC | GCT | TAC | GAG | CTC |
| 46  | GAG | AGC | TCG | TCT | GAG | GTG | ACG | TCG | TCT | TCA | GCA | CTG | GGC | CTG | CCG |
|     | CTC | TCG | AGC | AGA | CTC | CAC | TGC | AGC | AGA | AGT | CGT | GAC | CCG | GAC | GGC |
| 91  | CCG | GCT | ATG | GTG | ATG | TCC | CCG | GAA | TCG | CTC | GCG | TCG | CCC | GAG | ATC |
|     | GGC | CGA | TAC | CAC | TAC | AGG | GGC | CTT | AGC | GAG | CGC | AGC | GGG | CTC | TAG |
| 136 | GGC | GGC | CTG | GAG | CTG | TGG | GGC | TAC | GAC | GAT | GGC | ATC | ACT | TAC | AGC |
|     | CCG | CCG | GAC | CTC | GAC | ACC | CCG | ATG | CTG | CTA | CCG | TAG | TGA | ATG | TCG |
| 181 | ATG | GCA | CAG | TCG | CTG | GGC | ACC | TGC | ACC | ATG | GAG | CAG | CAG | CAG | CCC |
|     | TAC | CGT | GTC | AGC | GAC | CCG | TGG | ACG | TGG | TAC | CTC | GTC | GTC | GTC | GGG |

Fig.3 i.

226 CAG CCG CAG CAG CCG CAG CAG ACA CAA CCC CTA CCT TCC ATG  
GTC GGC GTC GTC GGC GTC GTC TGT GGT GGG GAT GGA AGG TAC

271 CCG TTA CCA ATG CCA CCG ACA ACA CCC AAA TCA GAA AAC GAG TCA  
GGC AAT GGT TAC GGT GGC TGT TGT GGT TTT AGT CTT TTG CTC AGT

316 ATG TCA TCA GGT CGT GAG GAA CTG TCT CCA GCT TCG AGT GTA AAC  
TAC AGT AGT CCA GCA CTC CTT GAC AGA GGT CGA AGC TCA CAT TTG

361 GGC TGC AGC ACA GAT GGC GAG GCG AGG CCG CAG AAG AAA GGC CCA  
CCG ACG TCG TGT CTA CCG CTC CGC TCC GCC GTC TTC TTT CCG GGT

406 GCG CCG AGG CAG CAA GAA GAG CTA TGT GTC TGC GGC GAC AGA  
CGC GGC TCC GTC GTC CTT CTC GAT ACA GAA CAG ACG CCG CTG TCT

451 GCC TCC GGA TAT CAC TAC AAC GCG CTC ACA TGT GAA GGG TGT AAA  
CGG AGG CCT ATA GTG ATG TTG CCG GAG TGT ACA CTT CCC ACA TTT

496 GGT TTC TTC AGG CCG AGT GTA ACC AAA AAT GCA GTG TAC ATA TGC



Fig.3 ii.

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CCA AAG AAG TCC GCC TCA CAT TGG TTT TTA CGT CAC ATG TAT ACG
541 AAA TTC GGC CAT GCT TGC GAA ATG GAT ATC TAT ATG CCG AGA AAA
TTT AAG CCG GTA CGA ACG CTT TAC CTA TAG ATA TAC GCC TCT TTT

586 TGT CAG GAG TGT CGG TTG AAG AAA TGT CTT GCG GTG GGC ATG AGG
ACA GTC CTC ACA GCC AAC TTC TTT ACA GAA CGC CAC CCG TAC TCC

631 CCC GAG TGC GTG GTG CCG GAG AAC CAG TGT GCA ATG AAA CGG AAA
GGG CTC ACG CAC CAC GGC CTC TTG GTC ACA CGT TAC TTT GCC TTT

676 GAG AAA AAG GCG CAG AGG GAA AAA GAC AAA TTG CCC GTC AGT ACG
CTC TTT TTC CGC GTC TCC CTT TTT CTG TTT AAC GGG CAG TCA TGC

721 ACG ACA GTA GAC GAT CAC ATG CCT CCC ATC ATG CAA TGT GAC CCT
TGC TGT CAT CTG CTA GTG TAC GGA GGG TAG TAC GTT ACA CTG GGA

766 CCG CCC CCA GAG GCG GCC GCT AGA ATT CTG GAA TGT GTG CAG CAC GAG
GGC GGG GGT CTC CGG CGA TCT TAA GAC CTT ACA CAC GTC GTG CTC

811 GTG GTG CCA CGA TTC CTG AAT GAG AAG CTA ATG GAA CAG AAC AGA
CAC CAC GGT GCT AAG GAC TTA CTC TTC GAT TAC CTT GTC TTG TCT

856 TTG AAG AAC GTG CCC CCC CTC ACT GCC AAT CAG AAG TCG TTG ATC
AAC TTC TTG CAC GCG GGG GAG TGA CGG TTA GTC TTC AGC AAC TAG

901 GCA AGG CTC GTG TGG TAC CAG GAA GGC TAT GAA CAA CCT TCC GAG
CGT TCC GAG CAC ACC ATG GTC CTT CCG ATA CTT GTT GGA AGG CTC

946 GAA GAC CTG AAG AGG GTT ACA CAG TCG GAC GAG GAC GAA GAC
CTT CTG GAC TTC TCC CAA TGT GTC AGC CTG CTC CTG CTT CTG

```

Fig.3 iii.

|      |  |
|------|--|
| 991  | TCG GAT ATG CCG TTC CGT CAG ATT ACC GAG ATG ACG ATT CTC ACA<br>AGC CTA TAC GGC AAG GCA GTC TAA TGG CTC TAC TGC TAA GAG TGT |
| 1036 | GTG CAG CTC ATC GTA GAA TTC GCT AAG GGC CTC CCG GGC TTC GCC<br>CAC GTC GAG TAG CAT CTT AAG CGA TTC CCG GAG GGC CCG AAG CGG |
| 1081 | AAG ATC TCG CAG TCG GAC CAG ATC ACG TTA TTA AAG GCG TGC TCA<br>TTC TAG AGC GTC AGC CTG GTC TAG TGC AAT TTC CGC ACG AGT     |
| 1126 | AGT GAG GTG ATG ATG CTC CGA GTG GCT CGG TAT GAC GCG GCC<br>TCA CTC CAC TAC TAC GAG GCT CAC CGA GCC ATA CTG CGC CGG         |
| 1171 | ACC GAC AGC GTA CTG TTC GCG AAC AAC CAG GCG TAC ACT CGC GAC<br>TGG CTG TCG CAT GAC AAG CGC TTG TTC GTC CGC ATG TGA GCG CTG |
| 1216 | AAC TAC CGC AAG GCA GGC ATG GCG TAC GTC ATC GAG GAC CTG CTG<br>TTG ATG GCG TTC CGT CCG TAC CGC ATG CAG TAG CTC CTG GAC GAC |
| 1261 | CAC TTC TGT CGG TGC ATG TAC TCC ATG ATG ATG GAT AAC GTG CAT<br>GTG AAG ACA GCC ACG TAC ATG AGG TAC TAC TAC CTA TTG CAC GTA |
| 1306 | TAT GCG CTG CTT ACA GCC ATT GTC ATC TTC TCA GAC CGG CCC GGG<br>ATA CGC GAC GAA TGT CGG TAA CAG TAG AAG AGT CTG GCC CCC     |
| 1351 | CTT GAG CAA CCC CTG TTG GTG GAG GAC ATC CAG AGA TAT TAC CTG<br>GAA CTC GTT GGG GAC AAC CAC CTC CTG TAG GTC TCT ATA ATG GAC |
| 1396 | AAC ACG CTA CGG GTG TAC ATC CTG AAC CAG AAC AGC GCG TCG CCC<br>TTG TGC GAT GCC CAC ATG TAG GAC TTG GTC TTG TCG CGC AGC GGG |
| 1441 | CGC GGC GCC GTC ATC TTC GGC GAG ATC CTG GGC ATA CTG ACG GAG  |

Fig.3 iv.

GCG CCG CCG CAG TAG AAG CCG CTC TAG GAC CCG TAT GAC TGC CTC

1486 ATC CGC ACG CTG GGC ATG CAG AAC TCC AAC ATG TGC ATC TCC CTC  
TAG GCG TGC GAC CCG TAC TCG TCG AGG TTG TAC ACG TAG AGG GAG

1531 AAG CTG AAG AAC AGG AAG CTG CCG CCG TTC CTC GAG GAG ATC TGG  
TTC GAC TTC TTG TCC TTC GAC GGC AAG GAG CTC CTC TAG ACC

1576 GAC GTG GCG GAC GTG GCG ACG ACG CCG GTG GCG GCG GAG  
CTG CAC CGC CTG CAC CGC TGC TGC CGC TGC GGC CAC CGC CGC CTC

1621 GCG CCG GCG CCT CTA GCC CCC GCG CCC GCG CCG CCC GCG GCG  
CGC GCG CGC GGA GAT CGG GCG GCG GCG GCG GCG GCG GCG GCG

1666 ACC GTC TAG CGC GCC TCA GGA GAG AAC GCT CAT AGA CTG GCT AGT  
TGG CAG ATC GCG CGG AGT CCT CTC TCG CGA GTA TCT GAC CGA TCA

1711 TTT AGT GAA GTG CAC GGA CAC TGA CGT CGA CGT GAT CAA CCT ATT  
AAA TCA CTT CAC GTG CCT GTG ACT GCA GCT GCA CTA GTT GGA TAA

1756 TAT AAG GAC TGC GAA TTT TAC CAC TTA AGA GGG CAC ACC CGT ACC  
ATA TTC CTG ACG CTT AAA ATG GTG AAT TCT CCC GTG TGG GCA TGG

1801 CGA TTT CGT ACG TAT TCG GTG ACC GAC GAC GAT GCA GAG CGT GTG  
GCT AAA GCA TGC ATA AGC CAC TGG CTG CTG CTA CGT CTC GCA CAC

1846 TAA TGT GAA TAT ATG TGT TGT TGA ACG ATT TGG AGA ATA TAT ATT  
ATT ACA CTT ATA TAC ACA ACA ACT TGC TAA ACC TCT TAT ATA TAA

1891 GGT GTT GCT GTT CGG GCC CGC ACG CCG TCG CCG GTC GGC GGC GAT  
CCA CAA CGA CAA GCC CGG GCG TGC GCG AGC GGC CAG CCG CCG CTA

Fig.3 v.

1936 CGC GGC GCC CGC GGC TTC AGT TTT ATT TCG TTT ACG ACT GAG TTG  
GCG CCG CGG CCG AAG TCA AAA TAA AGC AAA TGC TGA CTC AAC

1981 GTC ACT CGG ATA CGA CTG TAT GAT AAG ACT TCG TTC GAT AAG TAC  
CAG TGA GCC TAT GCT GAC ATA CTA TTC TGA AGC AAG CTA TTC ATG

2026 ACC TAC TAA ATT ACA CAT ACG TAC GTA GCT TAC GAG AGT TAT TAG  
TGG ATG ATT TAA TGT GTA TGC ATG CAT CGA ATG CTC TCA ATA ATC

2071 AGA CAA AGA ATA TAA GAA GAA GAT GTT TCT ATT GGG TGA AAA GTT  
TCT GTT TCT TAT TAT ATT CTT CTT CTA CAA AGA TAA CCC ACT TTT CAA

2116 GAT AGT TAT GTT TAT TTA CCA AAA TTA ACA ATA ATA CGT TGA TTA  
CTA TCA ATA CAA ATA AAT GGT TTT AAT TGT TAT TAT GCA ACT AAT

2161 ACC TTT CGA GTA TAA TAT TGT GAT GAG TCG TCC GCT GTC CAC GTC  
TGG AAA GCT CAT ATT ATA ACA CTA CTC AGC AGG CGA CAG GTG CAG

2206 GCC GTC ACA TGT TTG TTT CTG ATG CAC ACG TGA GGN GCG TTA TCG  
CGG CAG TGT ACA AAC AAA GAC TAC GTG TGC ACT CCN CGC AAT AGC

2251 TGT TTC ATG GTT CCA TCG TCC TGT GCC CGC GAC CCT CGA CTA AAT  
ACA AAG TAC CAA GGT AGC AGG ACA CGG GCG CTG GGA GCT TTA

2296 GAG TAA TTT AAT TTA TTG CTG TGA TTA CAT TTT AAT GTG TTG ATT  
CTC ATT AAA TTA AAT AAC GAC ACT AAT GTA AAA TTA CAC AAC TAA

2341 ATC TAC CAT AGG GTG ATA TAA GTG TGT CTT ATT ACA ATA CAA AGT  
TAG ATG GTA TCC CAC TAT ATT CAC ACA GAA TAA TGT TAT GTT TCA

2386 GTG TGT CGT CGA TAG CTT CCA CAC GAG CAA GCC TTT TGT TTA AGT

Fig.3 vi. CAC ACA GCA GCT ATC GAA GGT GTG CTC GTT CGG AAA ACA AAT TCA  
 2431 GAT TTA CTG ACA TGG ACA CTC GAC CCG GAA CTT C  
 CTA AAT GAC TGT ACC TGT GAG CTG GGC CTT GAA G

Total number of bases is: 2464.

Fig.4.

Sequence ID 4

|  |     |     |     |     |     |
|--|-----|-----|-----|-----|-----|
| 10   | 20  | 30  | 40  | 50  | 60  |
|  |     |     |     |     |     |
| <b>ACTCGCGTGCTCTTCTCACCTGTGCTCGGATTGTGTGTACTAGAAAAAGTTGTGCGCC</b>      |     |     |     |     |     |
| 70   | 80  | 90  | 100 | 110 | 120 |
|  |     |     |     |     |     |
| <b>GCTCGAACGAGACTTCCGAGTCCCTATTGGATTGCACGAAAGTCGACAGTGGAATAGCGA</b>    |     |     |     |     |     |
| 130  | 140 | 150 | 160 | 170 | 180 |
|  |     |     |     |     |     |
| <b>TTCCGGTTTCGTTTGAACGTTGCCGTAGACGAGTGGTGCATGTCCATGAGTCGCGGTTTAGAT</b> |     |     |     |     |     |

Fig.4 i.

190 | 200 | 210 | 220 | 230 | 240 |  
AGTTTAGTCCGAGGAAAGTGAAGTGAAGCCCTTCTCGGAGGATGTCCCTCGGGCGCTC  
M S L G A

250 | 260 | 270 | 280 | 290 | 300 |  
GTGGATACCGGAGGTGTGACACGCTCGCCGACATGAGACGCCCGCTGGTATAACAACGGAC  
R G Y R R C D T L A D M R R R W Y N N G

310 | 320 | 330 | 340 | 350 | 360 |  
CATTCCAGACGCTGCCGAATGCTCGAGGAGAGCTCGTCTGAGGTACGTCGCTTTCAGCAC  
P F Q T L R M L E E S S S E V T S S S A

370 | 380 | 390 | 400 | 410 | 420 |  
TGGGCCTGCCCGGCTATGGTGATGTCCCCGGAATCGCTCGCGTCCCGGAGATCGGGCG  
L G L P P A M V M S P E S L A S P E I G

Fig.4 ii.

430 | 440 | 450 | 460 | 470 | 480 |  
GCCTGGAGCTGTGGGGCTACGACGATGGCATCACTTACAGCATGGCACAGTCGCTGGGCA  
G L E L W G Y D D G I T Y S M A Q S L G  
490 | 500 | 510 | 520 | 530 | 540 |  
CCTGCACCATGGAGCAGCAGCAGCCCCAGCCGCAGCAGCAGCCGCAGCAGACACACAACCCC  
T C T M E Q Q Q P Q Q P Q Q Q P Q Q T Q P  
550 | 560 | 570 | 580 | 590 | 600 |  
TACCTTCCATGCCCGTTACCAATGCCACCGACAACACCCCAATCAGAAAACGAGTCAATGT  
L P S M P L P M P P T T P K S E N E S M  
610 | 620 | 630 | 640 | 650 | 660 |  
CATCAGGTCGTGAGGAACGTCTCCAGCTTCGAGTGTAACGGCTGCAGCACAGATGGCG  
S S G R E E L S P A S S V N G C S T D G  
670 | 680 | 690 | 700 | 710 | 720 |  
AGGCGAGGCGCAGAAAGGCCCGCCGAGGCGAGCAAGAGAGCTATGTCTTGTCT  
E A R R Q K K G P A P R Q Q E E L C L V

Fig.4 iii.

730 740 750 760 770 780  
| | | | |  
GCGGCACAGAGCCTCCGGATATCACTACAACGGCTCACATGTGAAGGTGTAAAGGTT  
C G D R A S G Y H Y N A L T C E G C K G

790 800 810 820 830 840  
| | | | |  
TCTTCAGGCGAGTGTAACCAAAATGCAGTGACATATGCAAATTCGGCCATGCTTCCG  
F F R R S V T K N A V Y I C K F G H A C

850 860 870 880 890 900  
| | | | |  
AAATGGATATCTATATCGGAGAAAATGTCAGGAGTGTGCGTTGAAGAAATGCTTTCGG  
E M D I Y M R R K C Q E C R L K K C L A

910 920 930 940 950 960  
| | | | |  
TGGGCATGAGGCCCGAGTGCCTGGTCCGGAGAACCAAGTGTGCAATGAAACGGAAAGAGA  
V G M R P E C V V P E N Q C A M K R K E

970 980 990 1000 1010 1020  
| | | | |  
AAAAGGCCAGAGGAAAAGACAAATTGCCCGTCAGTACGACGACAGTAGACGATCACA  
K K A Q R E K D K L P V S T T V D D H



Fig.4 iv.

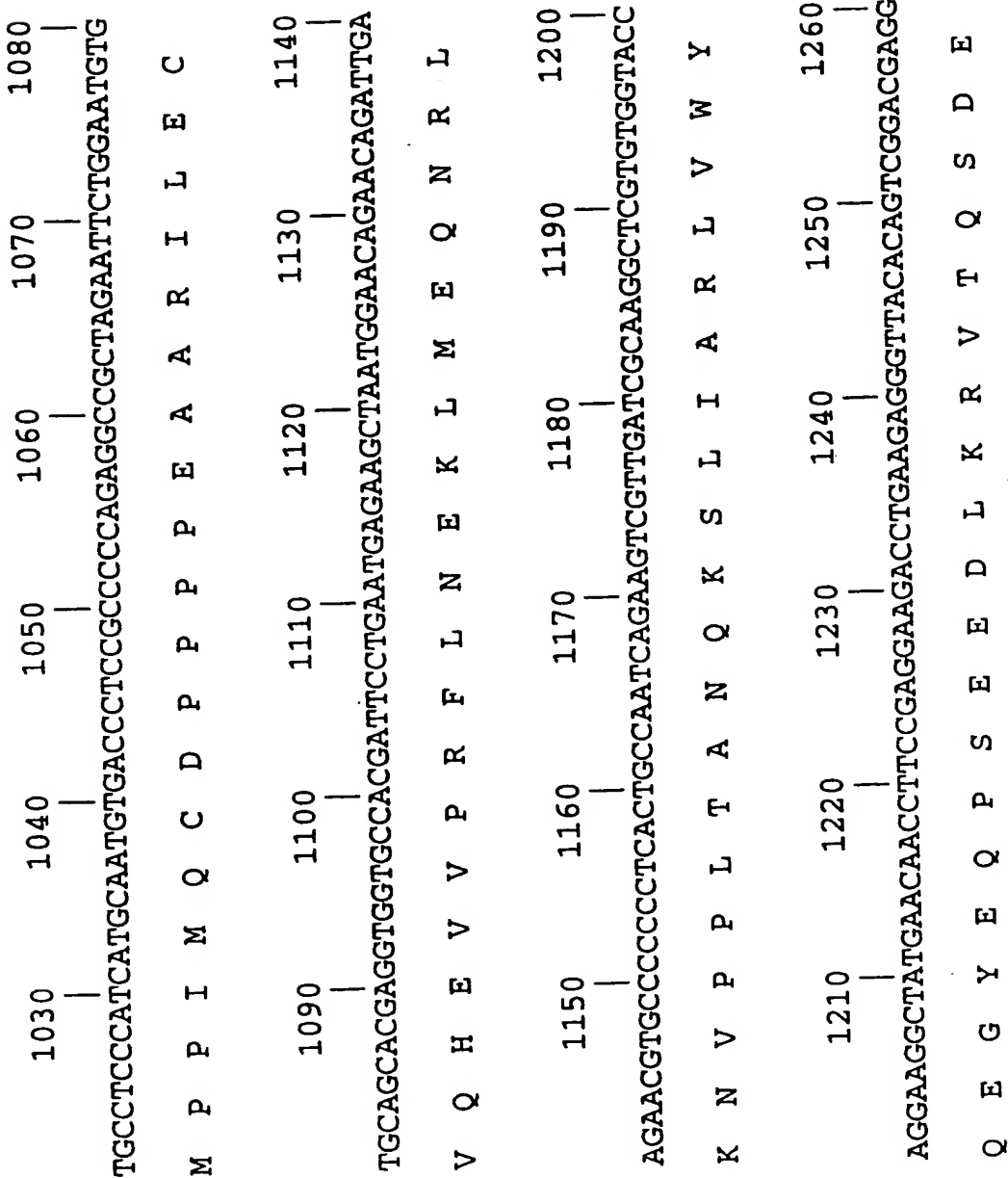


Fig.4 v.

1270 1280 1290 1300 1310 1320  
ACGACGAAGACTCGGATATGCCGTTCCGTCAGATTACCGAGATGACGATTCTCACAGTGC  
D D E D S D M P F R Q I T E M T I L T V  
1330 1340 1350 1360 1370 1380  
AGCTCATCGTAGAATTCGCTAAGGGCCTCCCGGGCTTCGCCAAGATCTCGCAGTCGGACC  
Q L I V E F A K G L P G F A K I S Q S D  
1390 1400 1410 1420 1430 1440  
AGATCACGTTATTAAAGGCGTGCTCAAGTGAGGTGATGATGCTCCGAGTGGCTCGGCGGT  
Q I T L L K A C S S E V M M L R V A R R  
1450 1460 1470 1480 1490 1500  
ATGACGGGCCACCGACAGCGTACTGTTCGCCGAACAACCGCGGTACACTCGCGACAAC  
Y D A A T D S V L F A N N Q A Y T R D N

Fig.4 vi.

1510 1520 1530 1540 1550 1560  
ACGCAAGGCAGGCATGGCGTACGTTCATCGAGGACCTGCTGCACTTCTGTCCGTGCATGT  
Y R K A G M A Y V I E D L L H F C R C M  
1570 1580 1590 1600 1610 1620  
ACTCCATGATGGATAACGTGCATTATGCGCTGCTTACAGCCATTGTCATCTTCTCAG  
Y S M M D N V H Y A L L T A I V I F S  
1630 1640 1650 1660 1670 1680  
ACCGCCCGGGCTTGAGCAACCCCTGTTGTGGAGGAGATCCAGAGATATTACCTGAACA  
D R P G L E Q P L L V E E I Q R Y Y L N  
1690 1700 1710 1720 1730 1740  
CGCTACGGGTGTACATCCTGAACCAGAACAGCGCGTCCGCCCGCGCGCGTCACTCTTCG  
T L R V Y I L N Q N S A S P R G A V I F

Fig.4 vii.

1750 1760 1770 1780 1790 1800  
GCGAGATCCTGGGCATACTGACGGAGATCCGCACGCTGGGCATGCAGAACTCCAACATGT  
G E I L G I L T E I R T L G M Q N S N M  
1810 1820 1830 1840 1850 1860  
GCATCTCCCTCAAGCTGAAGAACAGGAAGCTGCCGCCGTTCTCTCGAGGAGATCTGGGACG  
C I S L K L K N R K L P P F L E E I W D  
1870 1880 1890 1900 1910 1920  
TGGCGGACGTGGCGACGACGGCGACGCCGGTGGCGGCGGAGCGCCGCCCTCTAGCCCC  
V A D V A T T A T P V A A E A P A P L A  
1930 1940 1950 1960 1970 1980  
CCGCCCCCGCCCGCCCGCCGCCACCGTCTAGCGCGCCTCAGGAGAGAACGCTCATA  
P A P P A R P P A T V -  
1990 2000 2010 2020 2030 2040  
GACTGGCTAGTTTGTAGTGAAGTGCACGGACACTGACGCTCGACGCTGATCAACCTATTATA

Fig.4 viii.

2050 2060 2070 2080 2090 2100  
AGGACTGCGAATTTTACCACCTTAAGAGGGCACACCCGTACCCGATTTCGTACGTATTCGG  
2110 2120 2130 2140 2150 2160  
TGACCGACGACGATGCAGAGCGTGTGTAATGTGAATATATGTGTGTTGTTGAACGATTTCGA  
2170 2180 2190 2200 2210 2220  
GAATATATATTGGTGTGCTGTTTCGGGCCCCGCACGCCGTCGCCGCGGATCCGG  
2230 2240 2250 2260 2270 2280  
GCGCCCGCGGCTTCAGTTTATTTTCGTTTACGACTGAGTTGGTCACTCGGATACGACTGT  
2290 2300 2310 2320 2330 2340  
ATGATAAGACTTCGTTTCGATAAAGTACACCTACTACTAAATTACACATACGTACGTAGCTTACG  
2350 2360 2370 2380 2390 2400  
AGAGTTATTAGACACAAAGAAATATAAGAGAGATGTTTCTATTGGGTGAAAAGTTGATA

Fig.4 ix.

2410 | 2420 | 2430 | 2440 | 2450 | 2460 |  
GTTATGTTTATTACCAAAATTAACAATAATACGTTGATTAAACCTTTCGAGTATAATATT

2470 | 2480 | 2490 | 2500 | 2510 | 2520 |  
GTGATGAGTCGTCGCTGTCCACGTCGCCGTGCACATGTTTGTTCGTGATGCACACGTGAG

2530 | 2540 | 2550 | 2560 | 2570 | 2580 |  
GNGCGTTATCGTGTTCATGGTTCATCGTCCTGTGCCCGCACCCCTCCGACTAAATGAGT

2590 | 2600 | 2610 | 2620 | 2630 | 2640 |  
AATTAAATTTATGCTGTGATTACATTTTAAATGTGTGATTATCTACCATAGGGTGATAT

2650 | 2660 | 2670 | 2680 | 2690 | 2700 |  
AAGTGTGCTTATTACAATACAAAGTGTGTGTCGTCGATAGCTTCCACACGAGCAAGCCT

2710 | 2720 | 2730 | 2740 |  
TTTGTTTAAAGTGATTTACTGACATGGACACTCGACCCCGGAACCTTC

Fig.5.

Sequence I.D. 5

|       |   |     |  |
|-------|---|-----|--|
| BmECR | MRVENVDNVS  | 10  |  |
| MsECR | -----   |     |  |
| HvECR | M-----  | 1   |  |
| CtECR | -----   |     |  |
| AaECR | -----   |     |  |
| DmECR | -----   |     |  |
| BmECR | FALNGRADEWCMSVETRLDSLVRKSEVKAYVGGCPSVITDAGAYDALFD | 60  |  |
| MsECR | -----   |     |  |
| HvECR | -SLGARGYRRC-----DTLAD                             | 16  |  |
| CtECR | -----   |     |  |
| AaECR | -----   |     |  |
| DmECR | -----   |     |  |
| BmECR | M-RRRWSNNGGFP-LRMLEESSEVTSSA-LGLPPAMVMSPELASPEY   | 107 |  |
| MsECR | M-RRRWSNNGCFP-LRMFEESSSEVTSSA-FGMPAAMVMSPELASPEY  | 47  |  |
| HvECR | M-RRRWYNNGGFQTLRMLEESSEVTSSA-LGLPPAMVMSPELASPEI   | 64  |  |
| CtECR | M-K-----TENLIVTT-VKVEPLNYASQSF                    | 23  |  |
| AaECR | MMKRRWSNNGGFTALRMLDDSSSEVTSSAAL----GMTMSPNSLGSPNY | 46  |  |
| DmECR | M-KRRWSNNGGF--MRLPEESSEVTSSNGLVLP SGVNMSPSSLDSDHY | 47  |  |
|       | * . . . . *                                       |     |  |

Fig.5 i.

|       |                        |  |     |
|-------|------------------------|--|-----|
| BmECR | GALELW----             | SY-----                                    | 114 |
| MseCR | GGLELW----             | SY-----                                    | 55  |
| HvECR | GGLELW----             | GY-----                                    | 72  |
| CtECR | GDNNI----              | YGGAT----                                  | 33  |
| AaECR | DELELW-SSYEDNAYNGHSV-- | LSNGNNN-----                               | 78  |
| DmECR | CDNDKWL                | CGNESGFGSGNGHGLSQQQQSVITLAMHGCSSTLPAQTTIIP | 97  |

|       |   |                     |     |
|-------|---|---------------------|-----|
| BmECR | -----   | DDGITY              | 121 |
| MseCR | -----   | DETMN               | 61  |
| HvECR | -----   | DDGIT-              | 77  |
| CtECR | -----   | KKQRLSEDETMNH       | 46  |
| AaECR | -----   | ANLLMNGIVGNNNL----- | 98  |
| DmECR | INGNANGGSTNGQYVPGATNLGALANGMLNGFGNGMQQIQNGHGLIN | ...                 | 147 |

|       |  |                         |     |
|-------|--|-------------------------|-----|
| BmECR | NTAQSLLGACNMQQQLQP-----                          | QQHPAPPTLPTMP----       | 154 |
| MseCR | YPAQSLLGACNAPQQQQQ-----                          | QQQPSAQPLPSMP----       | 94  |
| HvECR | YSMAQSLGTCIMEQQQP-----                           | QQPQQTQPLPSMP----       | 114 |
| CtECR | NQTNMNLSSNMNHTIS-----                            | GFSSPDVNYEAYSPNSKL----- | 86  |
| AaECR | MASQAVQANANSIQHIVGN-----                         | LINGVNPNTLIPPLPS----    | 134 |
| DmECR | STTPSTPTTPLHLQQNLGGAGGGIGGMGILHHANGTPNGLIGVVGGGG |                         | 197 |

|       |   |   |     |
|-------|---|---|-----|
| BmECR | -----   | LPMPPTTPKSENESSGREETSPASSINGCSADA--D      | 190 |
| MseCR | -----   | LPMPPTTPKSENESSGREETSPASSINGCSTDG--E      | 130 |
| HvECR | -----   | LPMPPTTPKSENESSGREETSPASSVNGCSTDG--E      | 146 |
| CtECR | MSVHMGDG-----                                     | LDG-----                                  | 98  |
| AaECR | -----   | IIQNTLMNTPRSESVNSISSGREDLSPSSSLNGYT--DGSD | 173 |
| DmECR | VGLGVGGGVGGLGMQHTPRSDSVNSISSGRDDLSPSSSLNGYSANESCD | *   | 247 |



**BmECR**  
**MSECR**  
**HvECR**  
**CtECR**  
**AaECR**  
**DmECR**

ARRQKKGPAPRQOEELCLVCGDRASGYHYNALTCEGCKGFFRRSVTKNAV  
 PRRQKKGPAPRQOEELCLVCGDRASGYHYNALTCEGCKGFFRRSVTKNAV  
 ARRQKKGPAPRQOEELCLVCGDRASGYHYNALTCEGCKGFFRRSVTKNAV  
 KSSSKKGPVPRQOEELCLVCGDRASGYHYNALTCEGCKGFFRRSVTKNAV  
 AKKQKKGPTPRQOEELCLVCGDRASGYHYNALTCEGCKGFFRRSVTKNAV  
 AKKSKKGPAPRVQOEELCLVCGDRASGYHYNALTCEGCKGFFRRSVTKSAV

\* \* \*

YICKFGHACEMDMYMRKQCERLKKCLAVGMRPECV IQEPS-KNKDRQR  
YICKFGHACEMDMYMRKQCERLKKCLAVGMRPECVVP ESTCKNKRREK  
YICKFGHACEMDMYMRKQCERLKKCLAVGMRPECV VPENQCAMKRKEK  
YICKFGHACEMDI YMRKQCERLKKCLAVGMRPECV VPENQCAMKRKEK  
YCCKFGHECEMDMYMRKQCERLKKCLAVGMRPECV VPENQCAIKRKEK  
YCCKFGHACEMDMYMRKQCERLKKCLAVGMRPECV VPENQCAIKRKEK  
YCCKFGHACEMDMYMRKQCERLKKCLAVGMRPGCV VPGNQCAMKRREK

+ + + + + \* \* \* \* \*

Y C K F G R A C E M D M I H N A C X Z

QKKDKGILLPVSTTTV-----EDHMPPIMQC  
EAQREKDKLPVSTTTV-----DDHMPAIMQC  
KAQREKDKLPVSTTTV-----DDHMPPIMQC  
KAQKEKDKVPGIVGNTSSSLLNQSLNNGSLKNLEISYREELLQQLMKC  
KAQKEKDKVQTNAT-----VSTTNTY-RS-----EILPILMKC  
KAQKEKDKMTTSPSSQHGNGSLASGGQDFVKK-----EILD-LMTC  
KAQKEKDKMTTSPSSQHGNGSLASGGQDFVKK-----EILD-LMTC \* \*

•  
•  
•  
•  
•

DPPPPEAARI-----HEVVPRYLSEKLMEQNQRQKNIPPLSANQKSLIARL  
 DPPPPEAARI-----HEVVPFRFLTEKLMEQNRLKNVTPLSANQKSLIARL  
 DPPPPEAARILECVQHEVVPFRFLNEKLMEQNRLKNVPPLTANQKSLIARL  
 DPPPHPMQQL-----PEKLLMENRAKGTQPOLTANQVAVIYKL  
 DPPPHQAIPLL-----PEKLLQENRLRNIPLLTANQMAVIYKL  
 EPPQHATIPLL-----PDEILAKCQARNIPSLTYNQLAVITKL  
 \* \* \* \* \*

[illegible]

•  
•  
•  
•  
\*  
\*  
•

**BmECR**  
**MsECR**  
**HvECR**  
**CtECR**  
**AaECR**  
**DmECR**

Fig.5 iii.

409  
351  
368  
334  
392  
474

VWYQEGYEQPSDEDLKRVTTWQ-SDEEDEESDLPFRQITEMTILTVQLI  
VMYQEGYEQPSEEDLKRVTTWQLEEEEEETDMPFRQITEMTILTVQLI  
VMYQEGYEQPSEEDLKRVTS---DEDDSDMPFRQITEMTILTVQLI  
IWYQDGVEQPSDEDLKRITTE--LEEEQDHEANFRYITEVTILTVQLI  
IWYQDGVEQPSDEDLKRIMIG--SPNEEQDQDVHFRHITEITILTVQLI  
IWYQDGVEQPSDEDLRRIM-S--QPDENESQTDVSRHITEITILTVQLI  
\*\* \*\*\*\* \* . . . . . \*\* \*\* \* \*\*\*\*

BmECR  
MsECR  
HvECR  
CtECR  
AaECR  
DmECR

459  
401  
418  
384  
442  
524

VEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARRYDAASDVLFANN  
VEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARRYDAATDVLFANN  
VEFAKGLPGFAKISQSDQITLLKACSSSEVMMLRVARRYDAATDVLFANN  
VEFAKGLPAFIKIPQEDQITLLKACSSSEVMMLRMARRYDHDSDSILFANN  
VEFAKGLPAFTKIPQEDQITLLKACSSSEVMMLRMARRYDAATDLSILFANN  
VEFAKGLPAFTKIPQEDQITLLKACSSSEVMMLRMARRYDHSDDSIFFANN  
\*\*\*\*\* \* \*\* \* \*\*\*\* \* \*\*\*\* \* \*\*\*\* \* . . . . . \*\*\*\*

BmECR  
MsECR  
HvECR  
CtECR  
AaECR  
DmECR

509  
451  
468  
434  
492  
574

KAYTRDNYRQGMAYVIEDLLHFCRCMFAMGMDNVHFALLTAIVIFS  
QAYTRDNYRKAGMSYVIEDLLHFCRCMYSMMDNVHYALLTAIVIFS  
QAYTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHYALLTAIVIFS  
TAYTKQTYQLAGMEETIDDLHFCRCQMYALSIDNVETALLTAIVIFS  
RSYTRDSYRMAGMADTIEDLLHFCRCQMFSLTVDNVEYALLTAIVIFS  
RSYTRDSYKMGAMADNIEDLLHFCRCQMFMSKVDNVEYALLTAIVIFS  
\*\*\*\*\* \* \*\* \* \*\*\*\* \* \*\*\*\* \* \*\*\*\* \* . . . . . \*\*\*\*

BmECR  
MsECR  
HvECR  
CtECR  
AaECR  
DmECR

559  
501  
518  
484  
542  
624

GLEQPSLVEEIQRYLNTLRIYIINQNSASSRCAVIYGRILSVLTELRTL  
GLEQPLLVVEEQRYLKTTLRVYILNQHSAPRCVLFKGILGVLTELRTL  
GLEQPLLVVEDIQRYLNTLRVYILNQNSASPRGAVIFGEILGILTEIRTL  
GLEKAEMVDIIQSYTETLKVYIVRDHGGESRCSVQFAKLLGILTELRTM  
GLEQAELVEHIQSVYIDTLRIYILNRHAGDPKCSVIFAKLLSILTELRTL  
GLEKAQLVEAIQSVYIDTLRITILNRHCGDSMSLVFYAKLLSILTELRTL  
\*\*\*\*\* \* \*\* \* \*\*\*\* \* \*\*\*\* \* \*\*\*\* \* . . . . . \*\*\*\*

BmECR  
MsECR  
HvECR  
CtECR  
AaECR  
DmECR

Fig.5 iv.

|       |  |     |
|-------|--|-----|
| BmECR | GTQNSNMCISLKLKNRKLPPFLEEIWDVAEVARR-----            | 593 |
| MseCR | GTQNSNMCISLKLKNRKLPPFLEEIWDVAEVSTT-----            | 535 |
| HvECR | GMQNSNMCISLKLKKRKLPPFLEEIWDVADVATT-----            | 552 |
| CtECR | GNLSEMCFSLKLNRNKLPRFLEEVDVGDVNNQTATTNTENIVRERIN    | 534 |
| AaECR | GNQSEMCFSLKLKNRKLPRFLEEIWDVDQDIPPSMQAQMHSHTQSSS--- | 590 |
| DmECR | GNQNAEMCFSLKLKNRKLPKFLEEIWDVHAIPPSVQSHLQITQEEDERLE | 674 |
|       | * * * * * . . . . . * * * * * . . . . .            |     |
| BmECR | -----  | 593 |
| MseCR | -----  | 535 |
| HvECR | -----  | 552 |
| CtECR | -----  | 536 |
| AaECR | RN-----  | 632 |
| DmECR | -----SSSSSSSSNGSSNGSSNSNSQHGPHPHGQQ--LTPNQ         | 724 |
|       | RAERMRAVGGAITAGIDCDSASTSAAAAAQHPQPQPQPSSLTQND      |     |
| BmECR | -----HPTV-----LPTNPVVL-----                        | 606 |
| MseCR | -----QP--TPGVAAQVTPIVVDNPAAL-----                  | 556 |
| HvECR | -----ATPVAAEAPAPLAPAPPARPATV-----                  | 575 |
| CtECR | -----  | 536 |
| AaECR | QQHQQQ-----HSQLQQ-----V                            | 645 |
| DmECR | SQHQTQPQLQPQLPPQLQGQLQPQLQTLQTLQPIQPQPQLLPVSAPV    | 774 |
| BmECR | -----  | 606 |
| MseCR | -----  | 556 |
| HvECR | -----  | 575 |
| CtECR | -----  | 536 |
| AaECR | HANGSGGGGNNSSSG-----                               | 663 |
| DmECR | PASVTAPGSLSAVSTSEYMGGSAAIGPITPATTSITAAVTASSTTSAPV  | 824 |

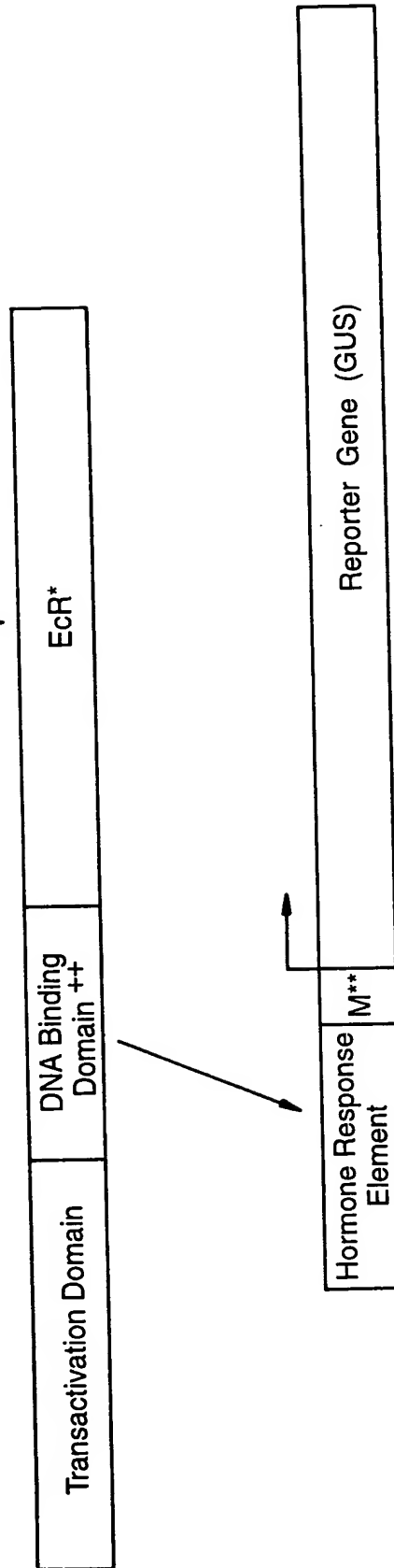
Fig.5 v.

|       |  |     |
|-------|--|-----|
| BmECR | -----  | 606 |
| MsECR | -----  | 556 |
| HvECR | -----  | 575 |
| CtECR | -----  | 536 |
| AaECR | -----GVVPGLGMLDQV-----                           | 675 |
| DmECR | PMGNGVGVGVGGNVSMYANAQTAMALMGVALHSHQQQLIGGVAVKSEH | 874 |

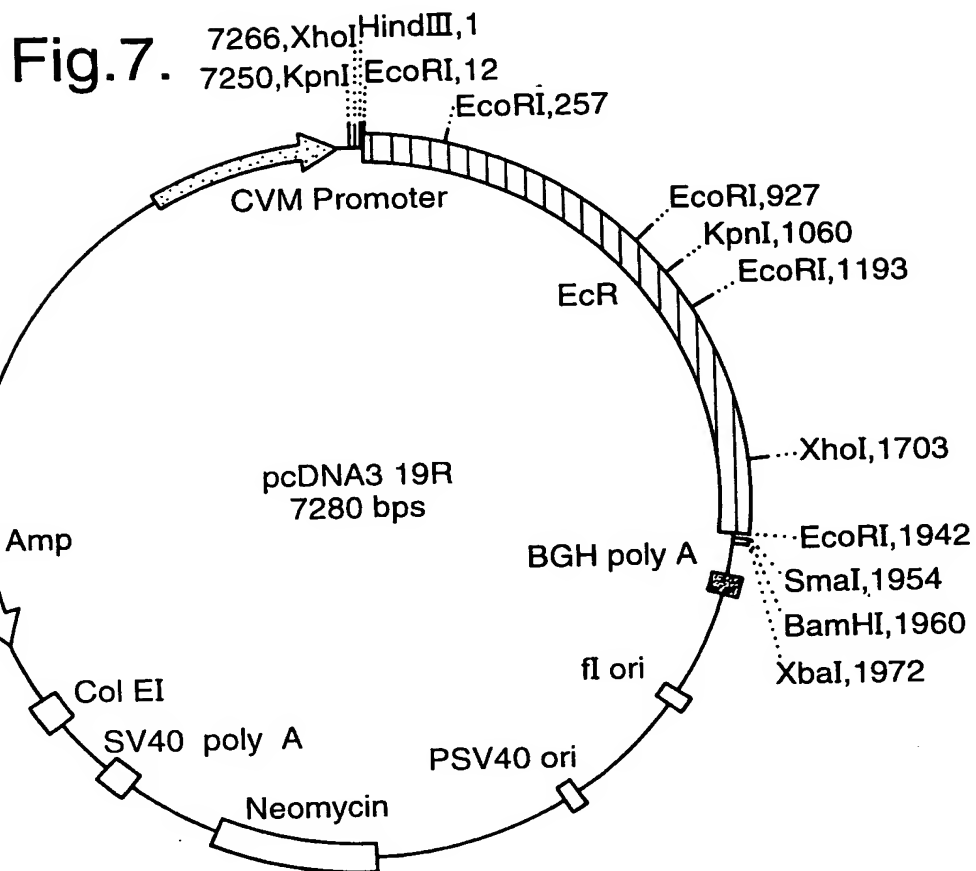
  

|       |      |     |
|-------|------|-----|
| BmECR | ---  | 606 |
| MsECR | ---  | 556 |
| HvECR | ---  | 575 |
| CtECR | ---  | 536 |
| AaECR | ---  | 675 |
| DmECR | STTA | 878 |

Fig.6. Chemical



- ++ Glucocorticoid receptor DNA binding and transactivation domains
- \* Insect ecdysone ligand binding domain
- \*\* Minimal 35S CaMV promoter



Response Element for HecR → → → →

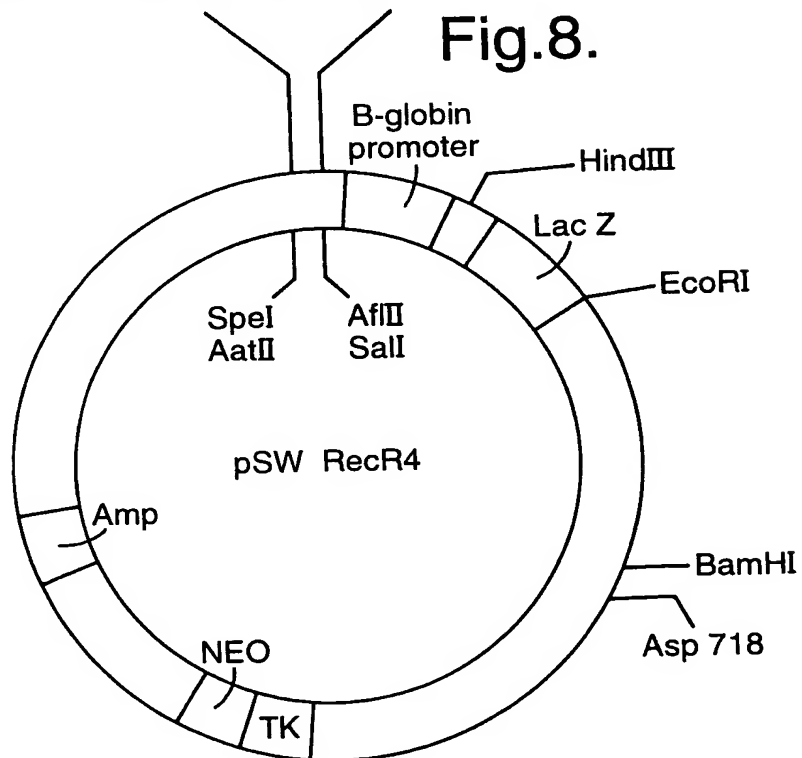


Fig.9.

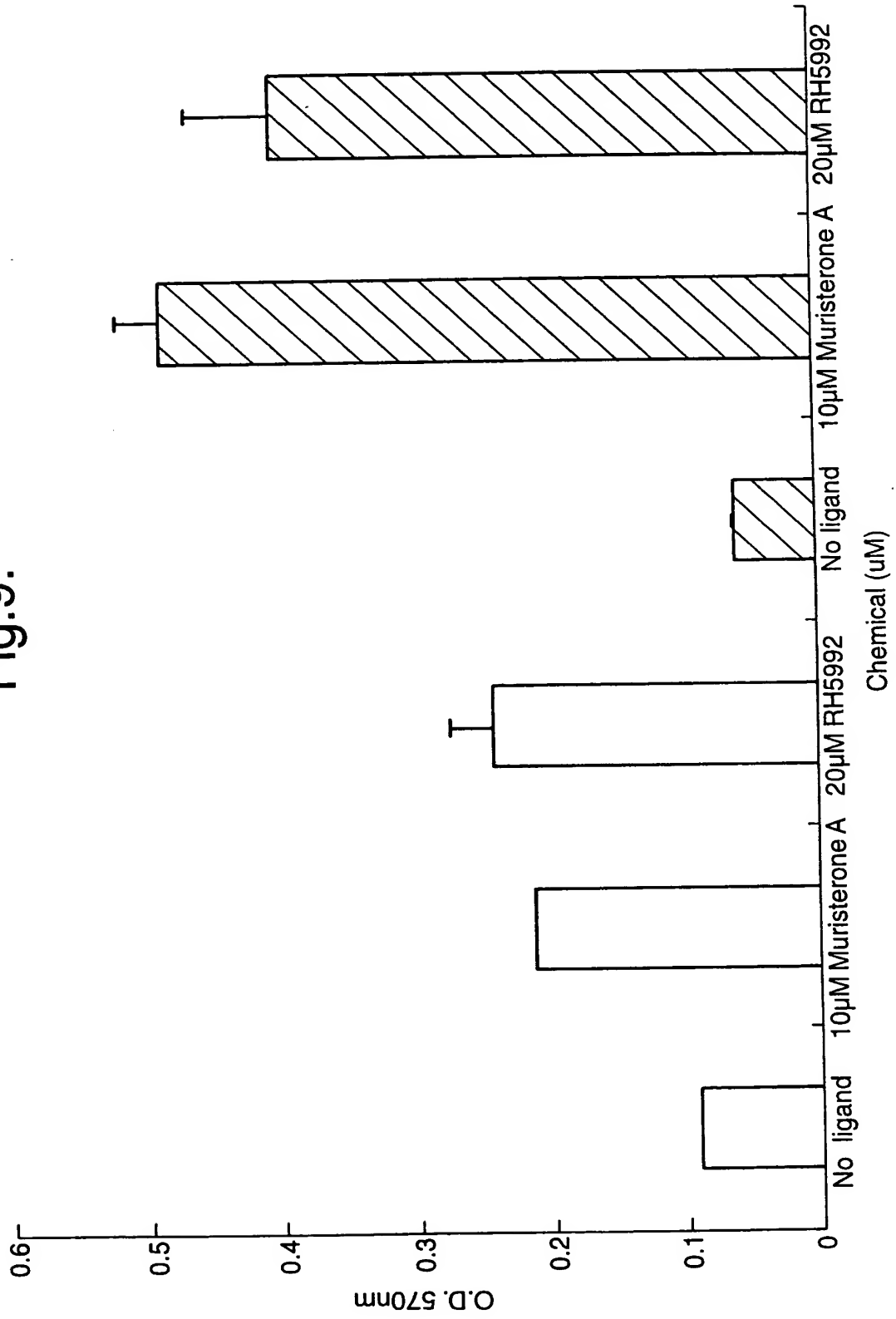


Fig.10.

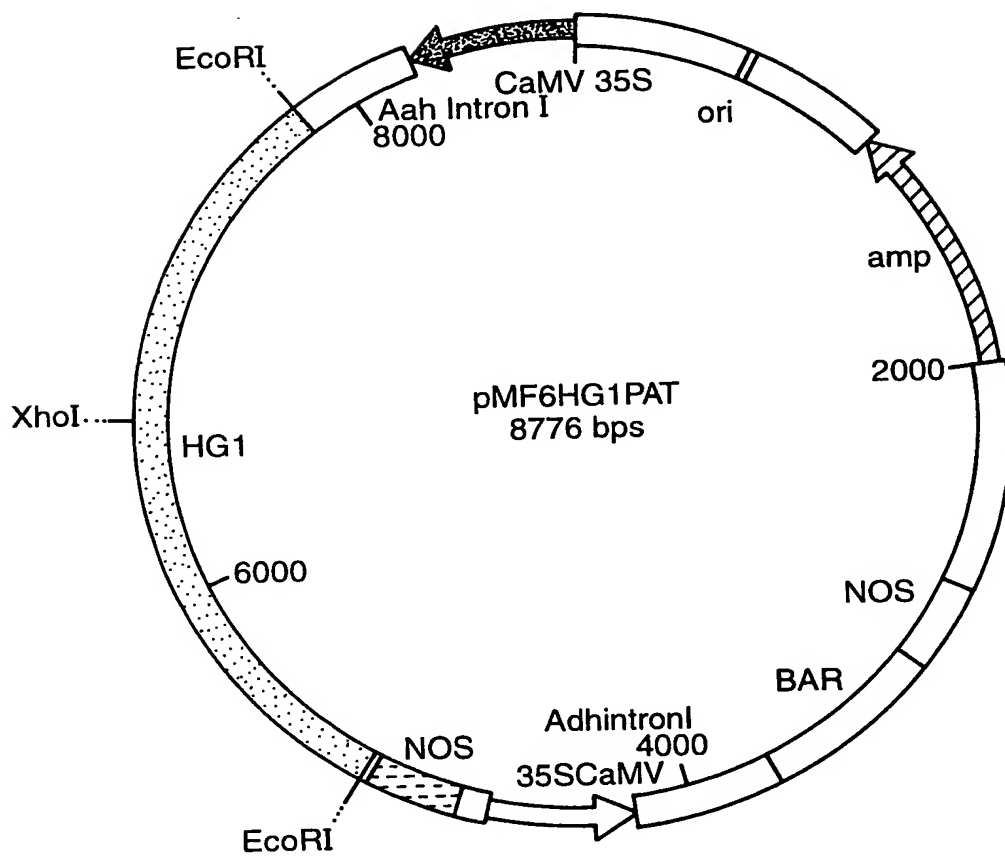




Fig.11.

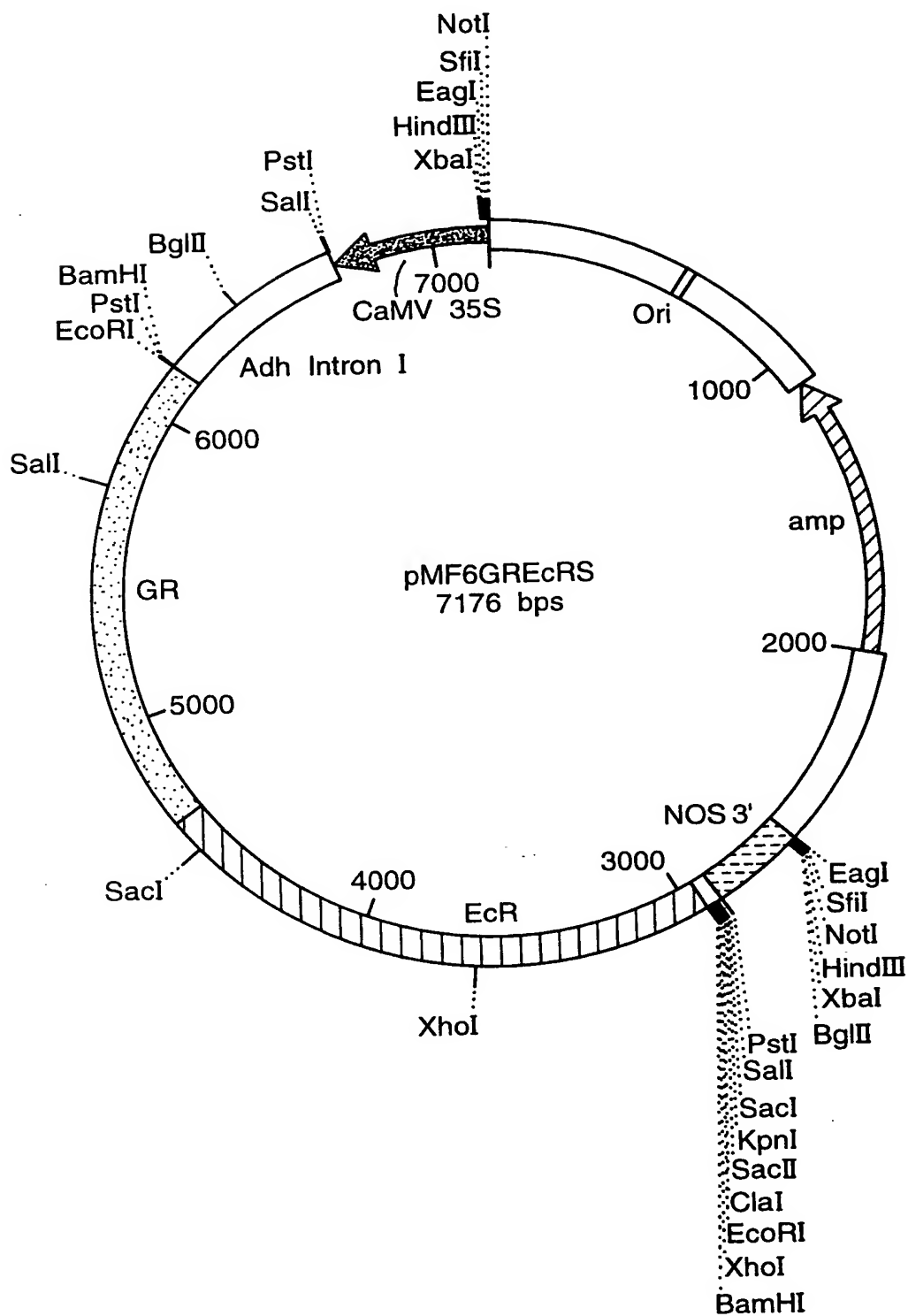


Fig.12.

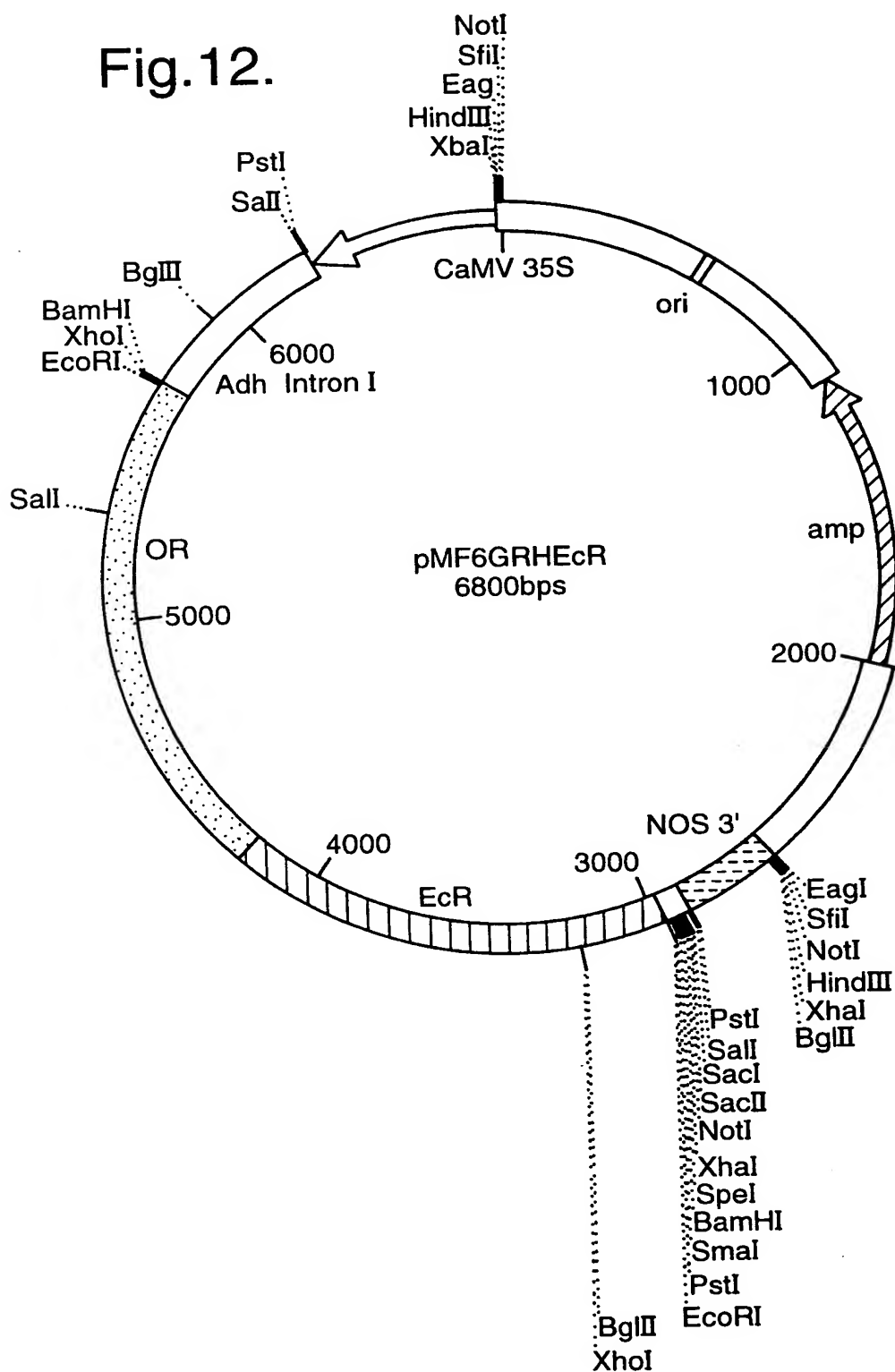


Fig.13.

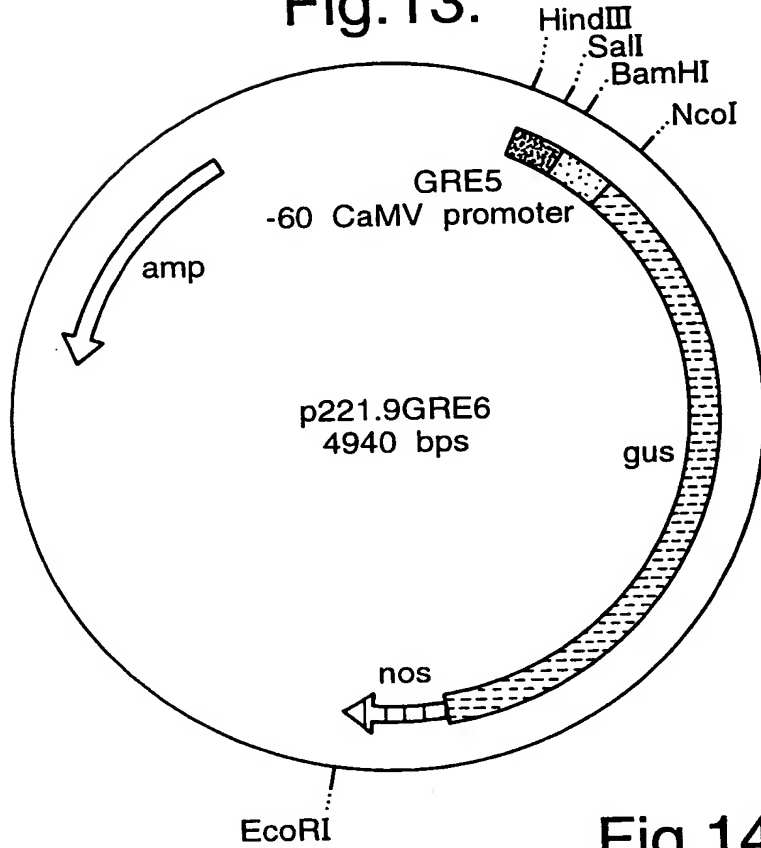


Fig.14.

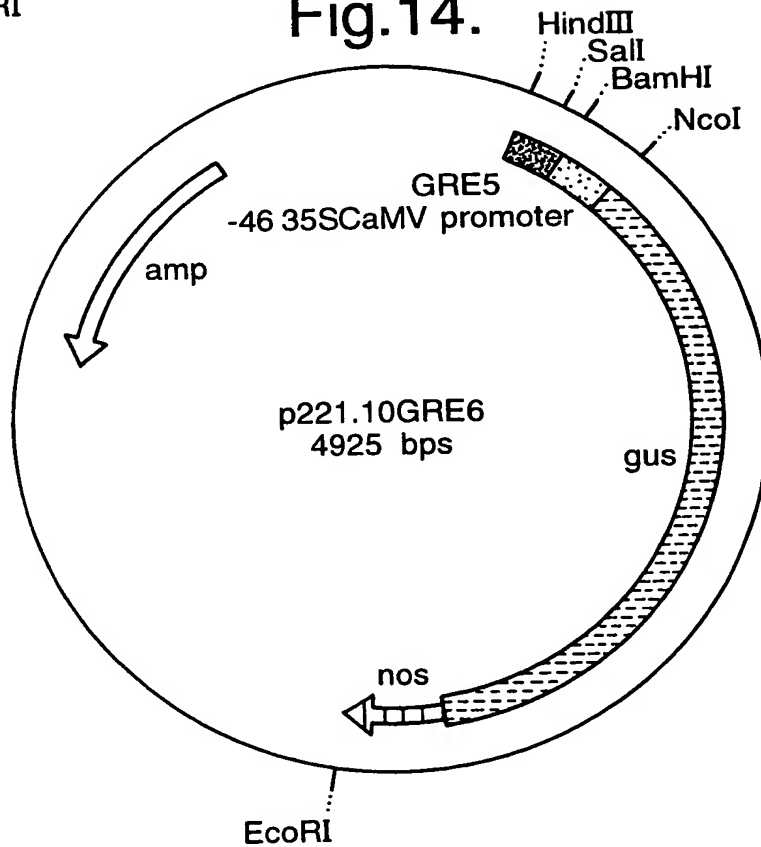


Fig.15.

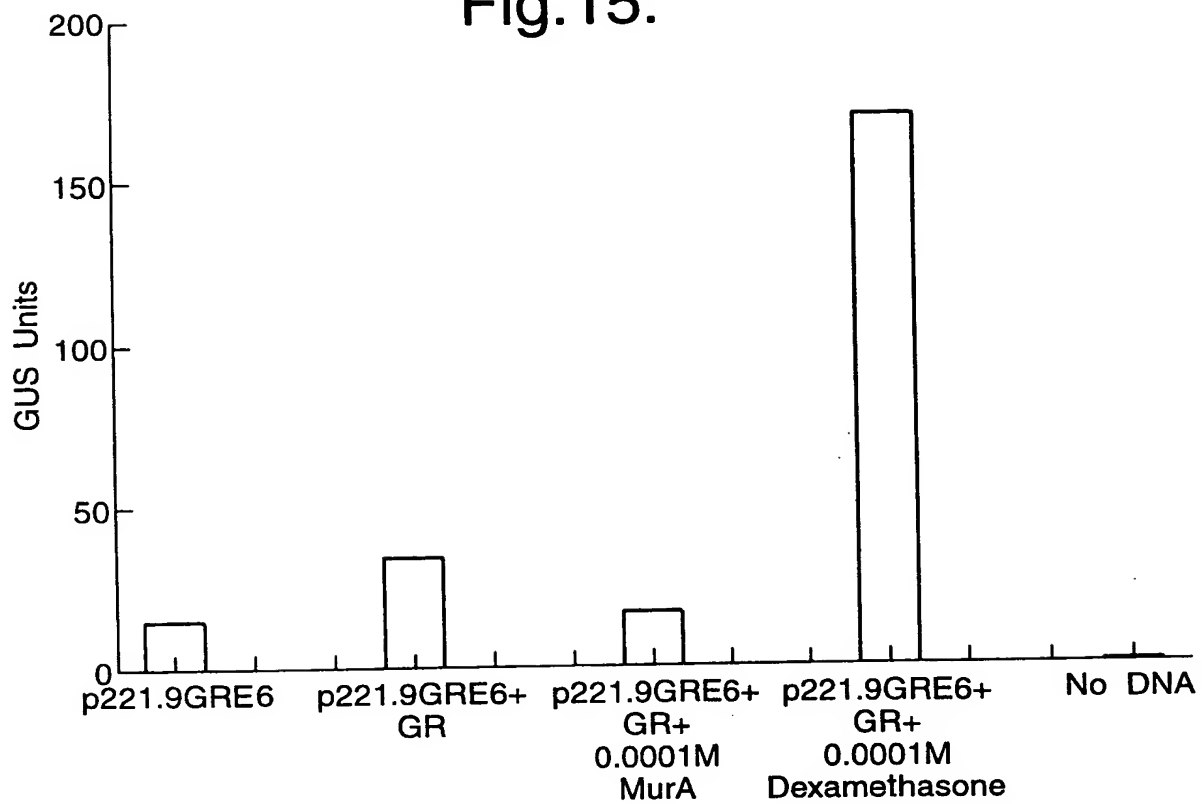


Fig.16.

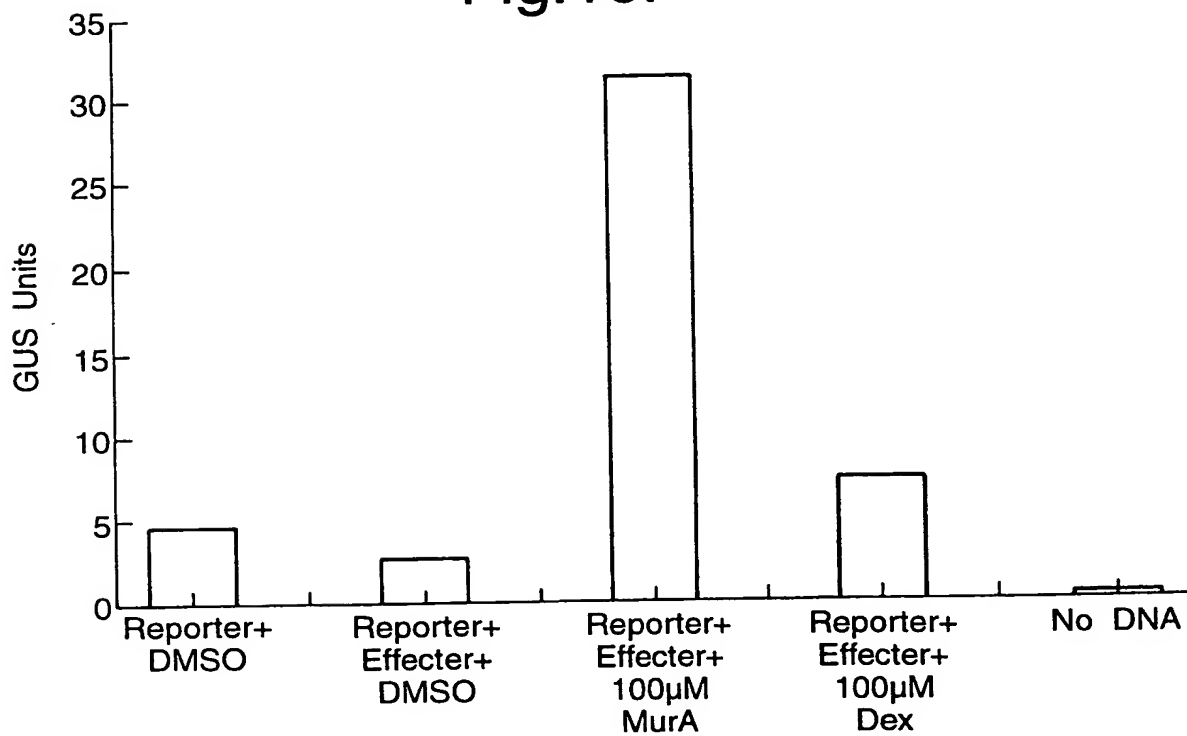


Fig.17.

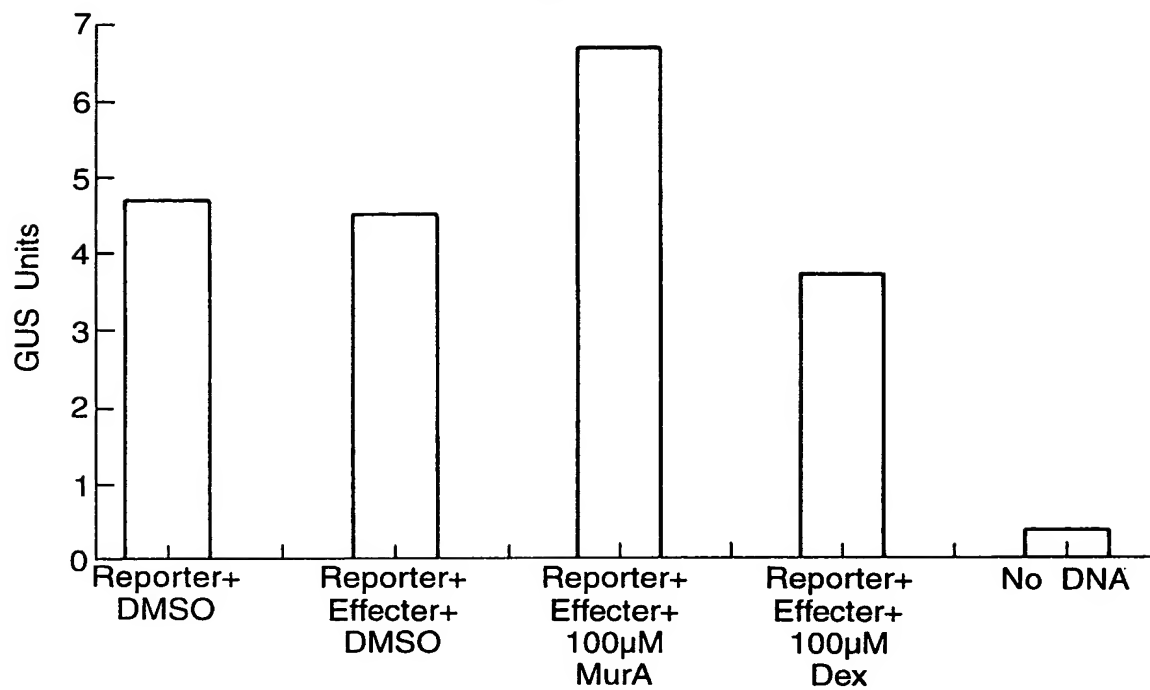


Fig.18.

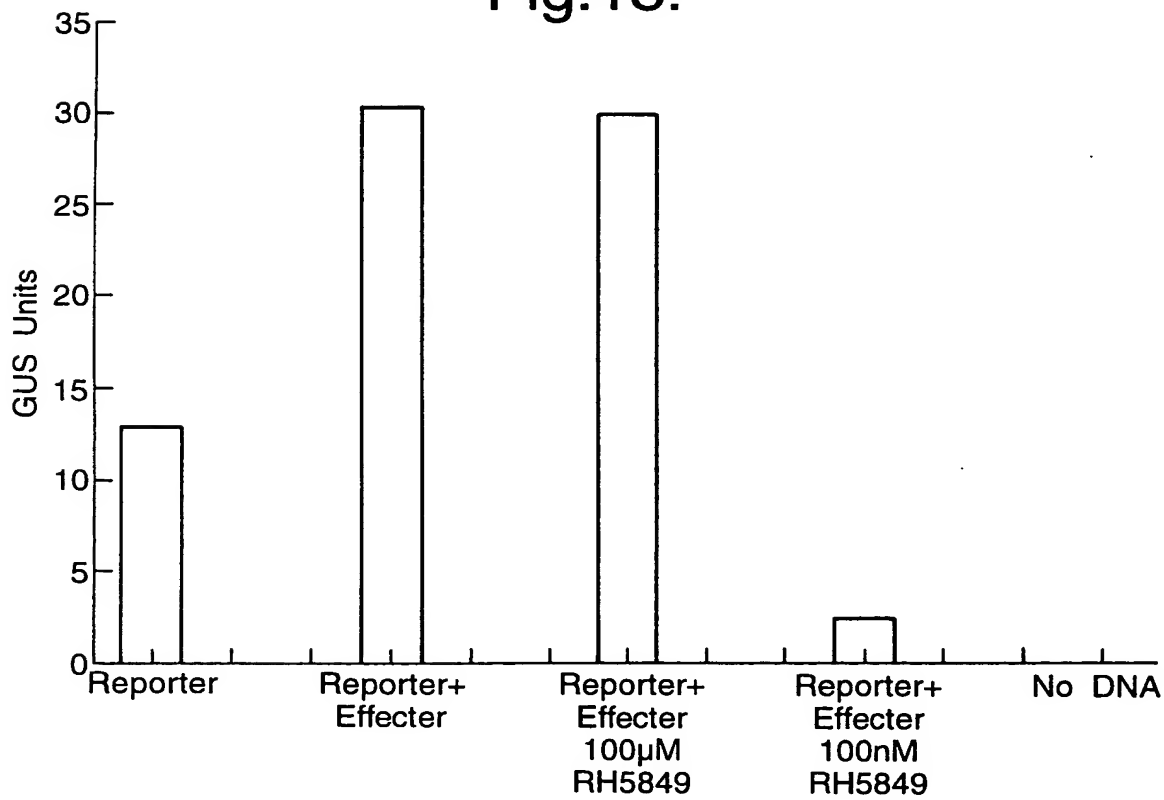


Fig.19.

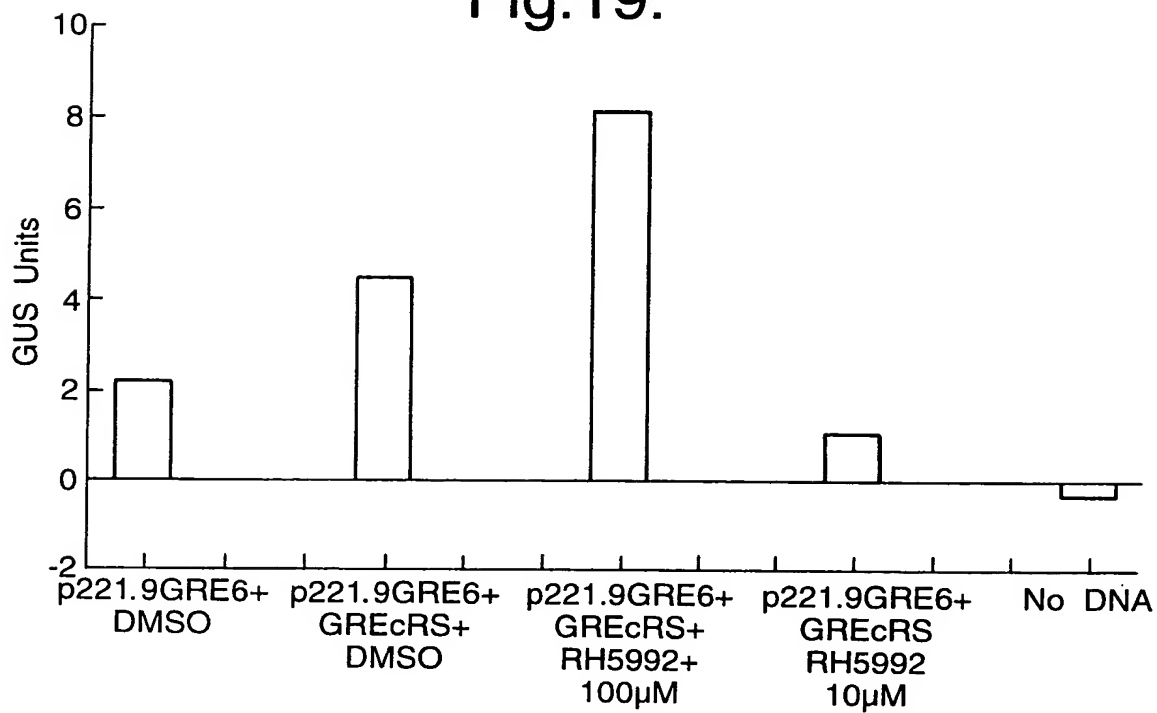
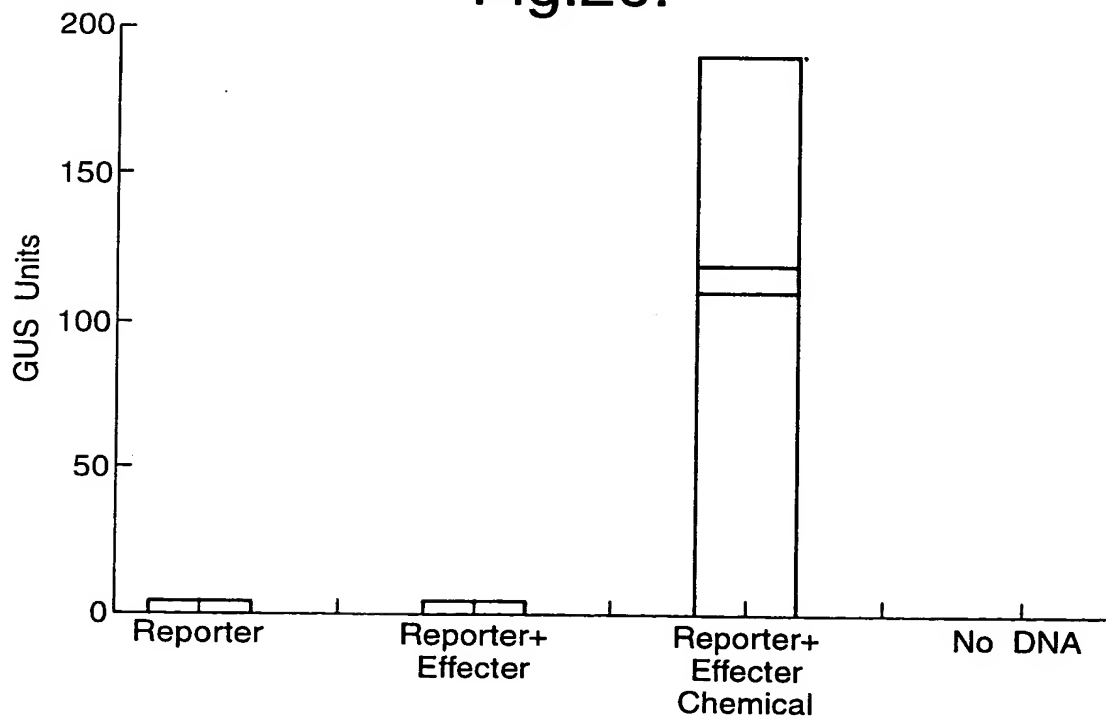


Fig.20.



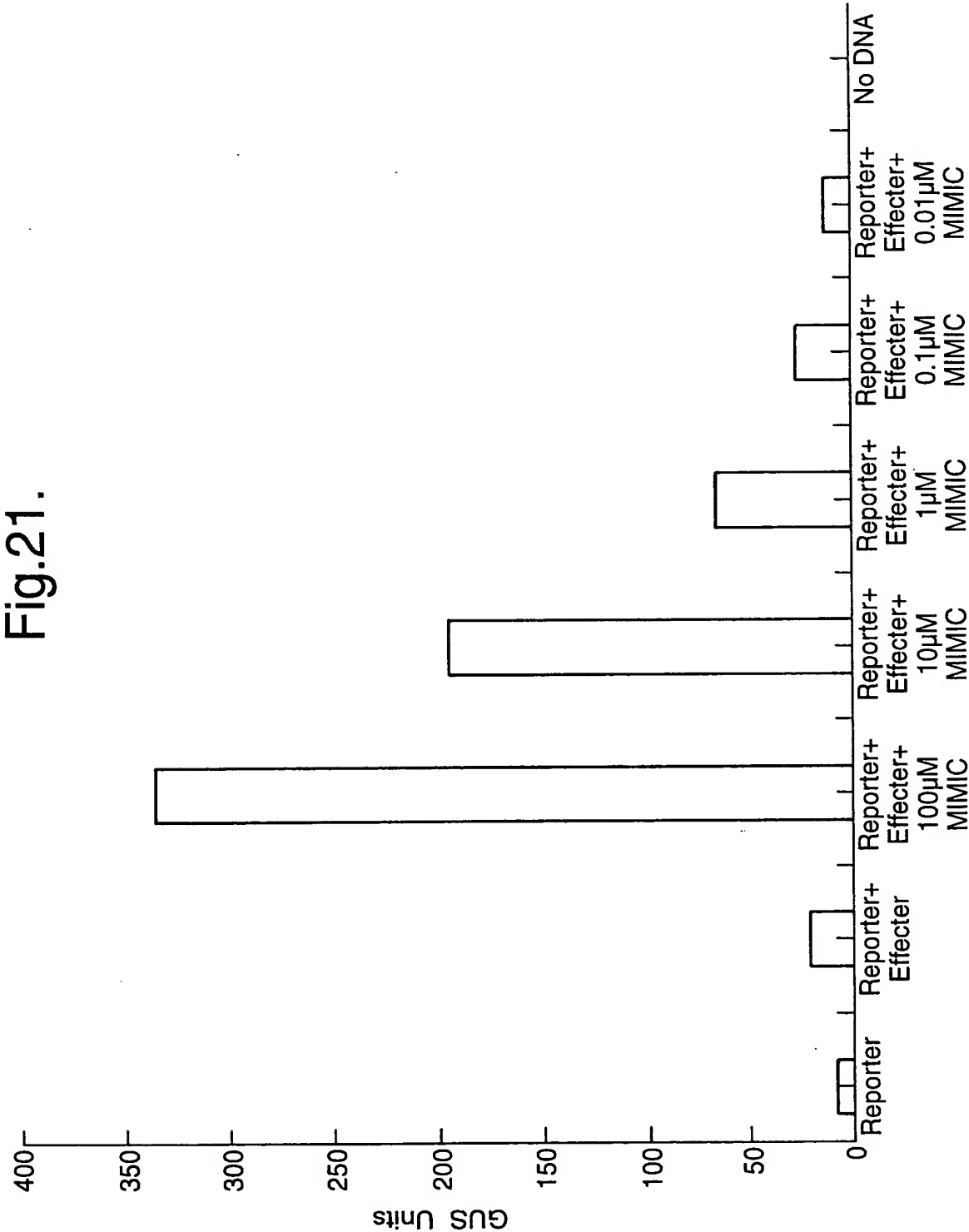


Fig.22.

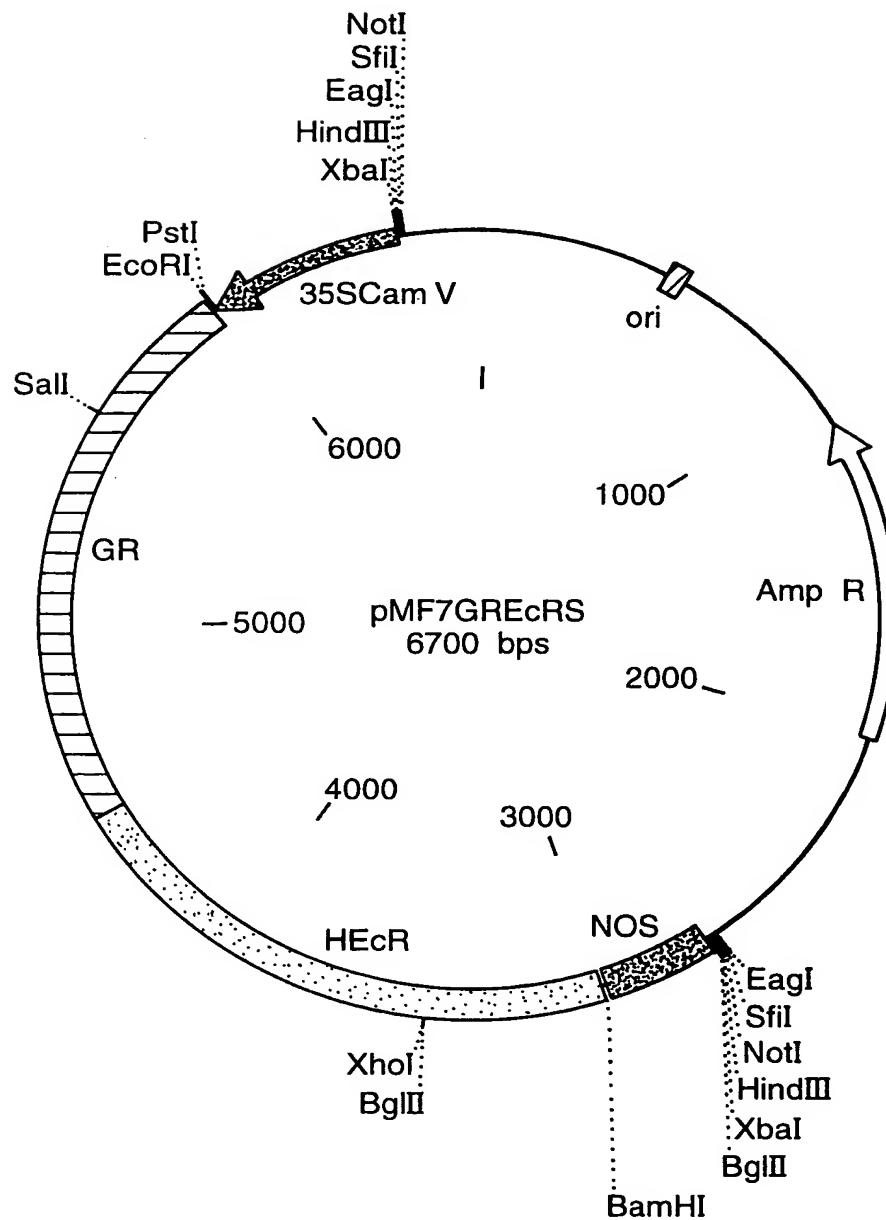




Fig.23.

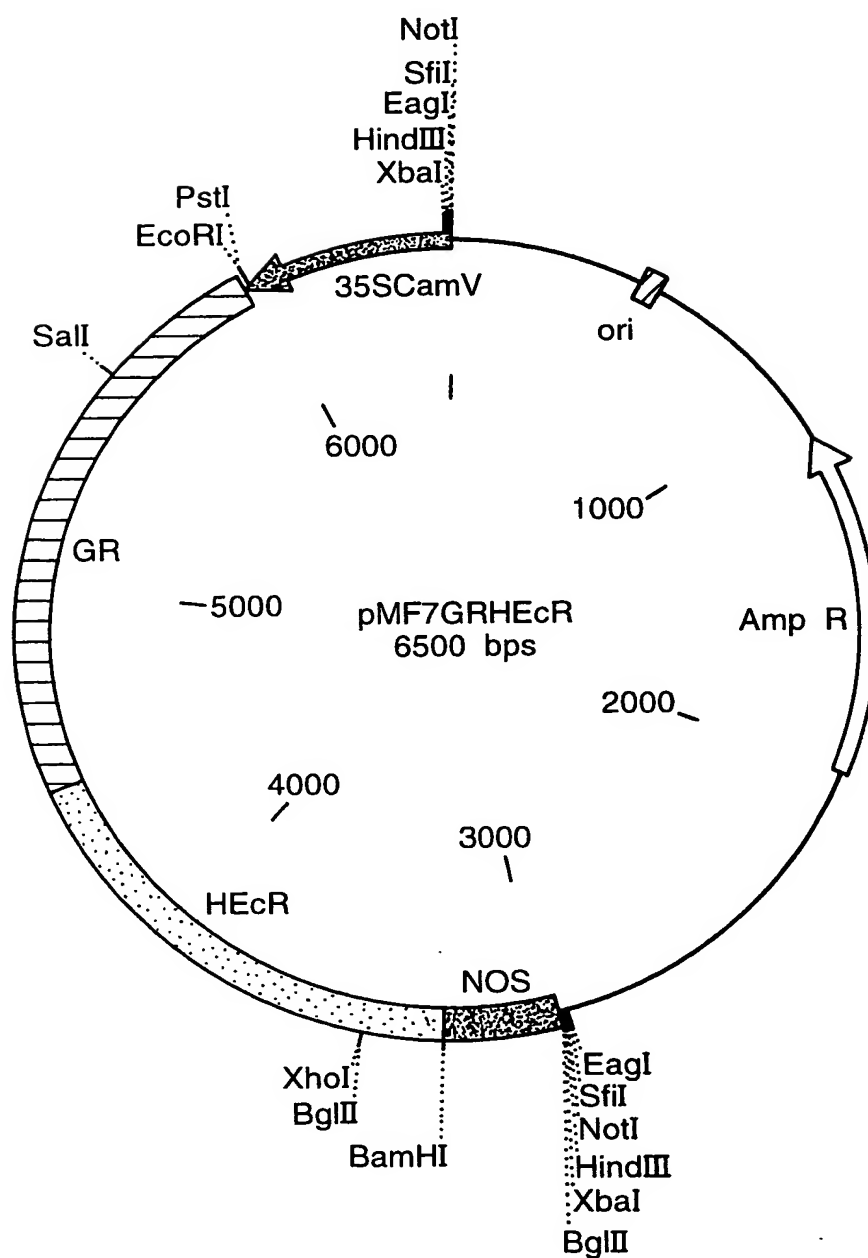


Fig.24.

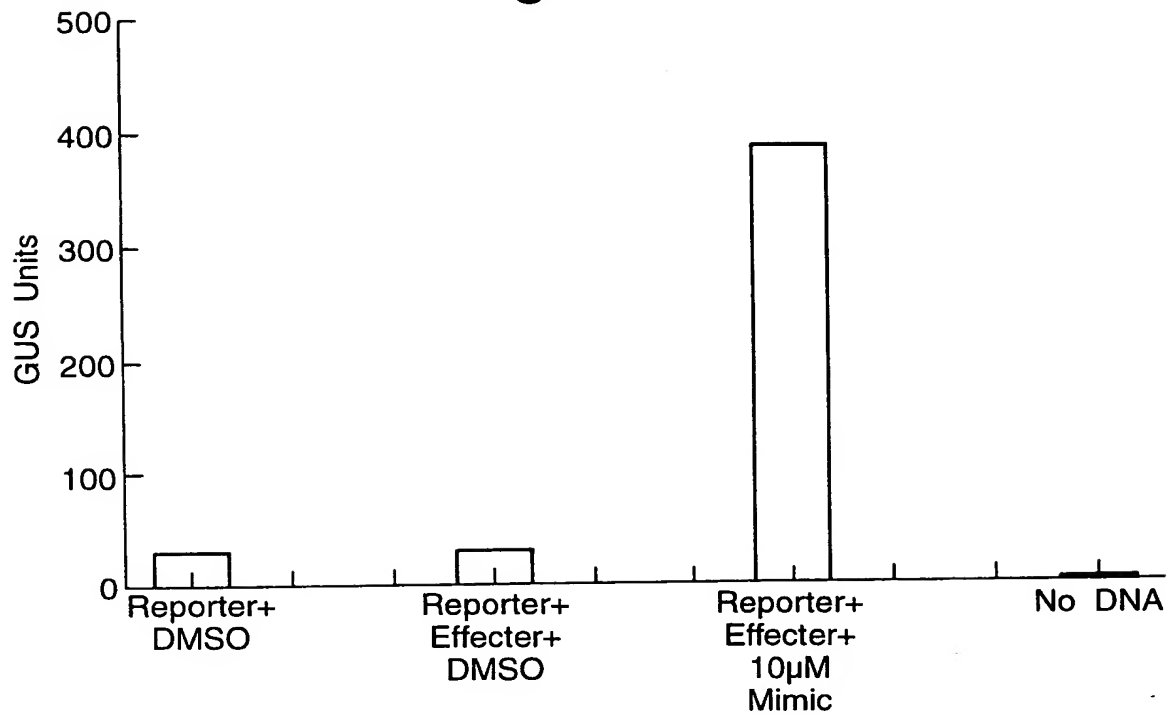


Fig.26.

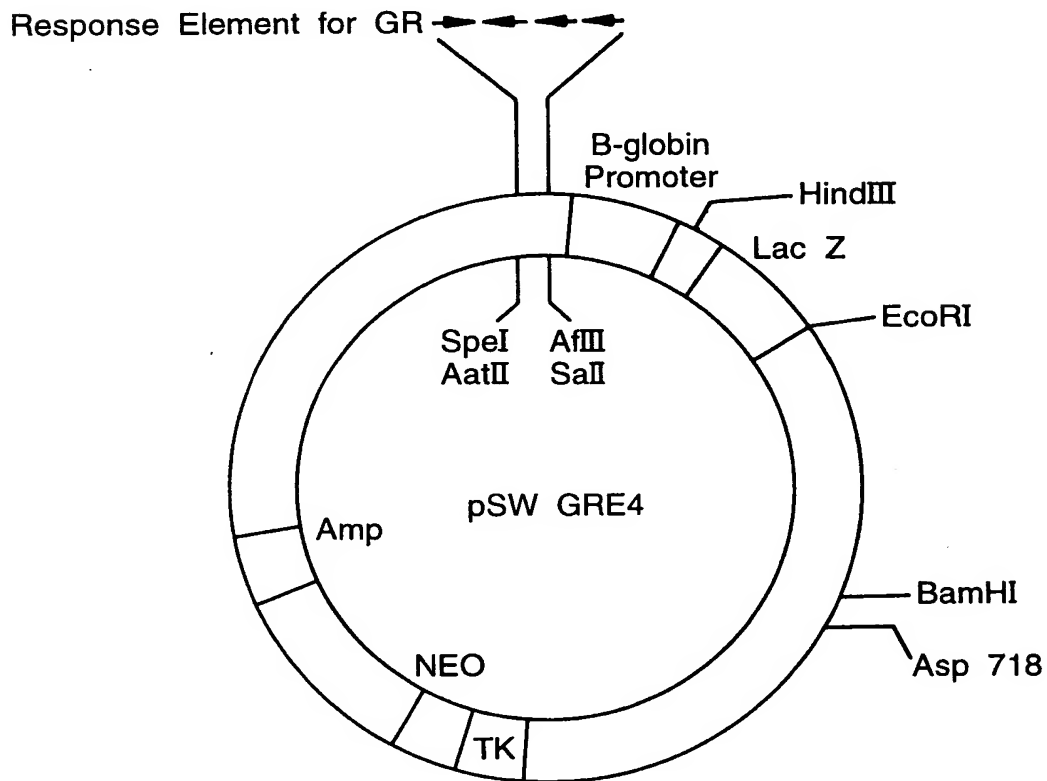


Fig.25.

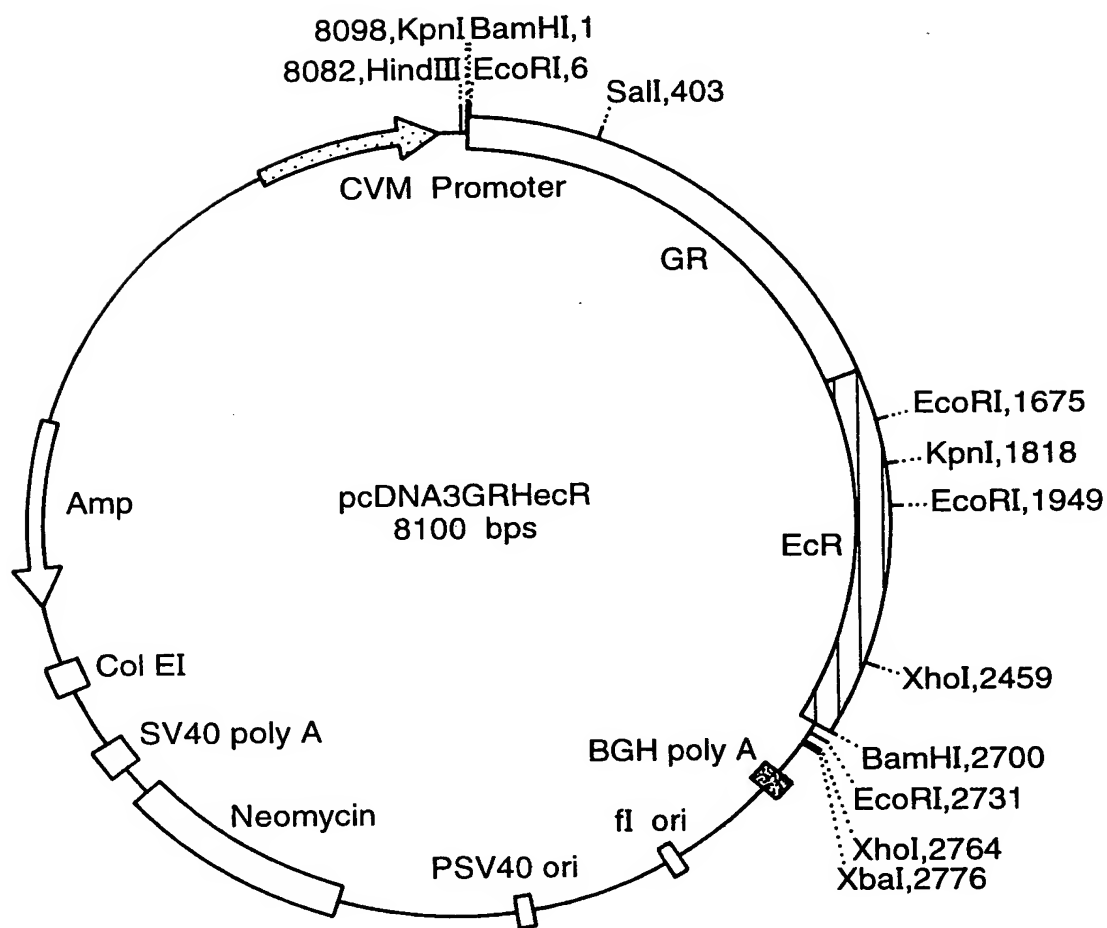


Fig.27.

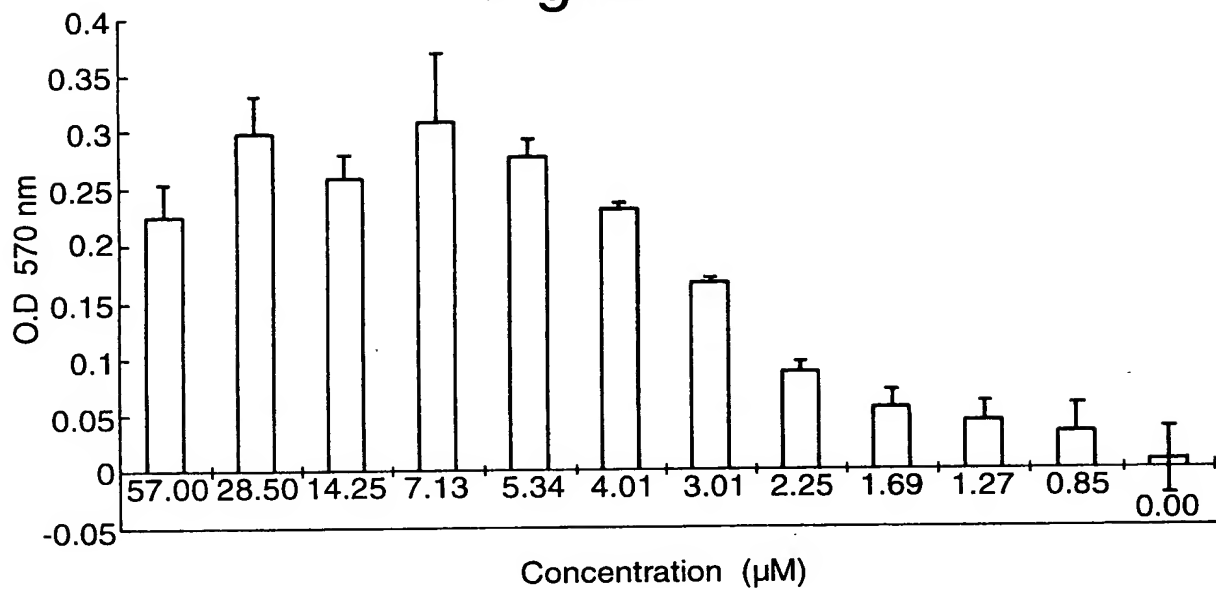


Fig.28.

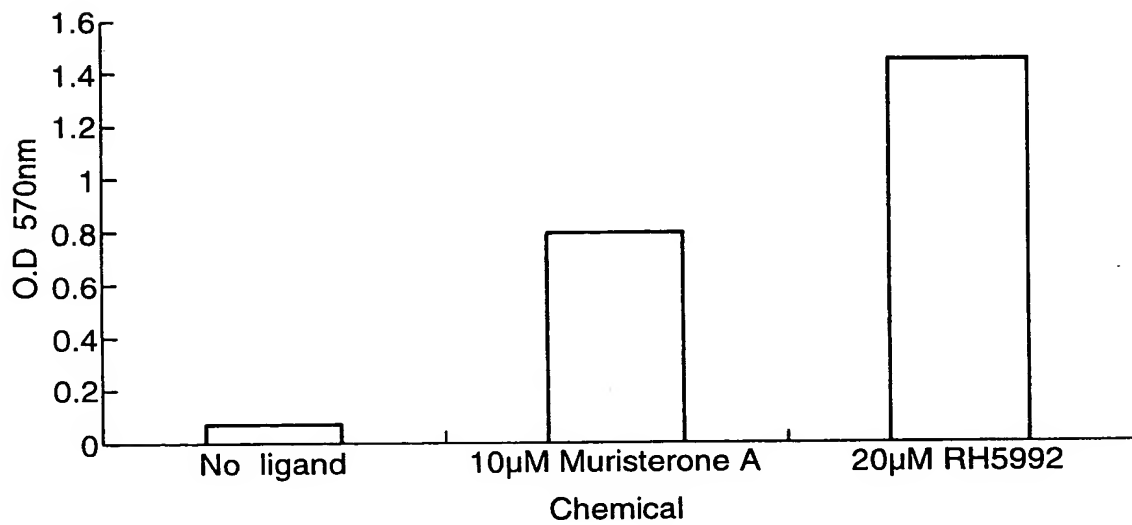


Fig.29.

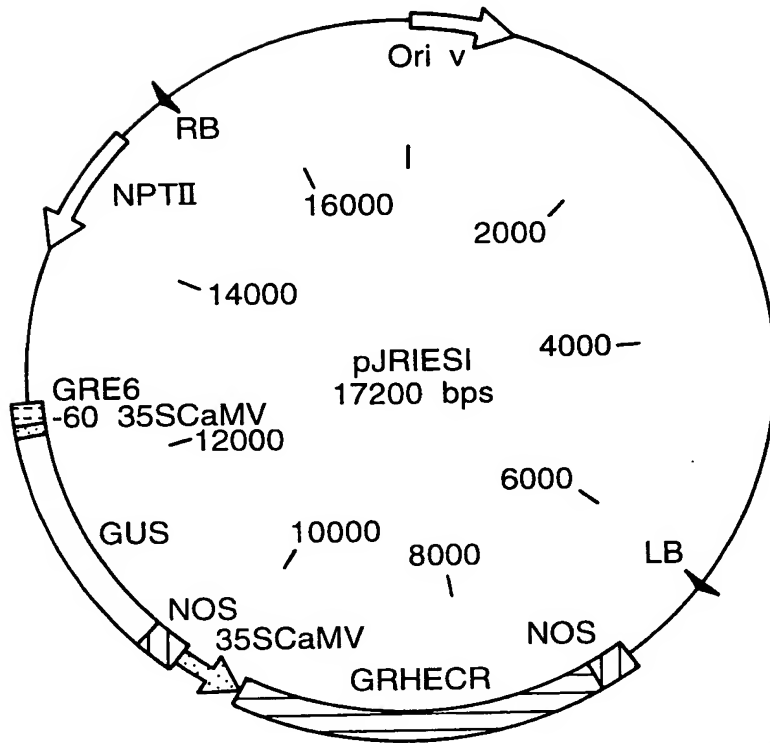


Fig.30.

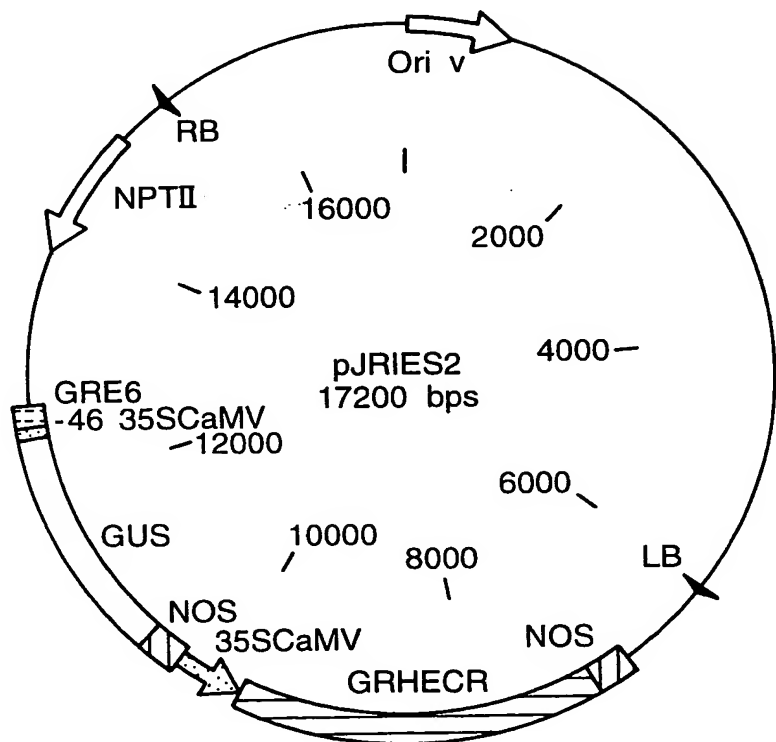


Fig.31.

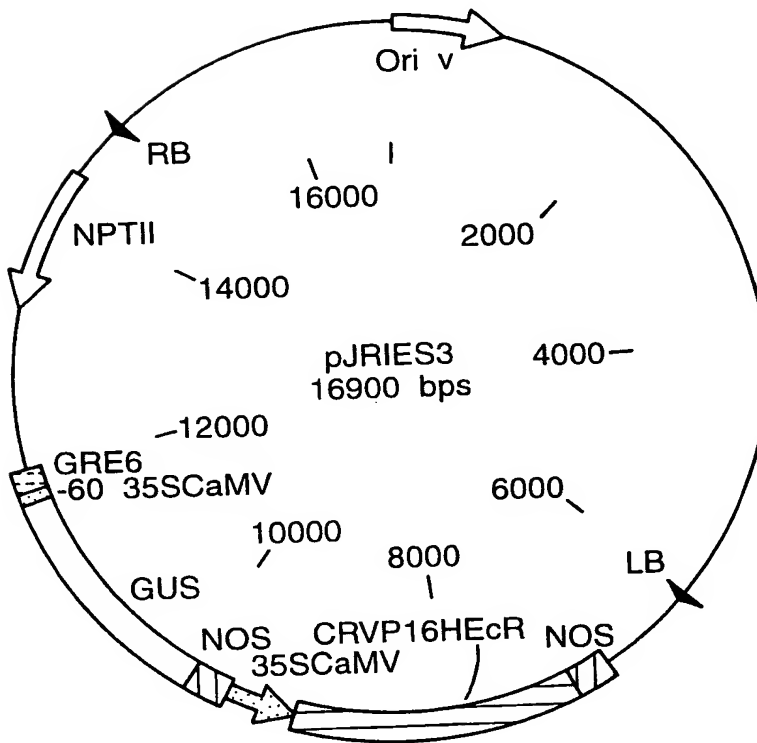


Fig.32.

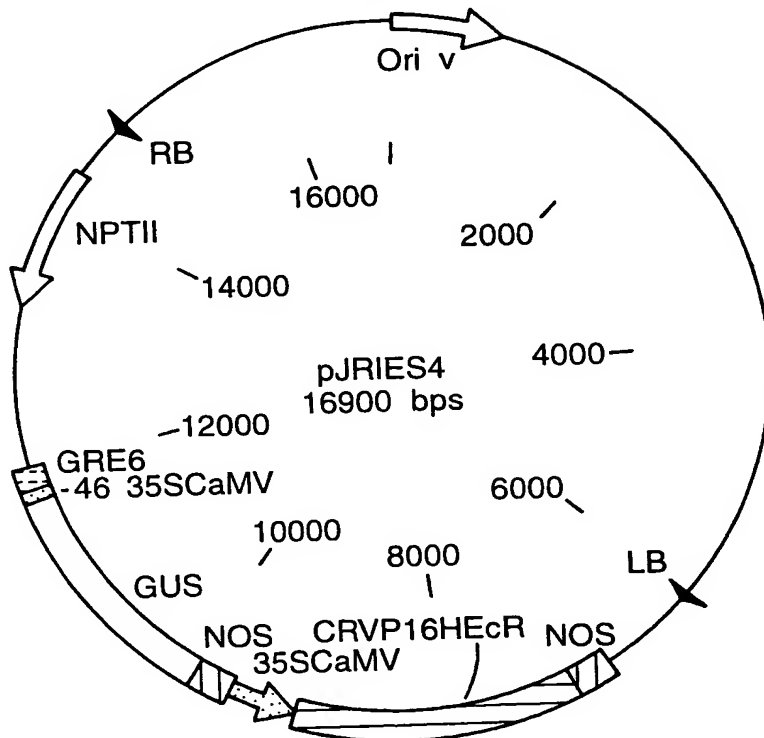


Fig.33.

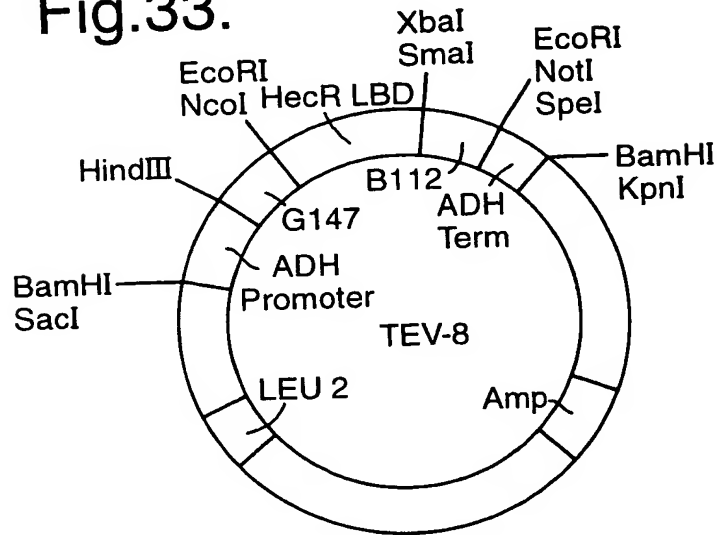


Fig.34.

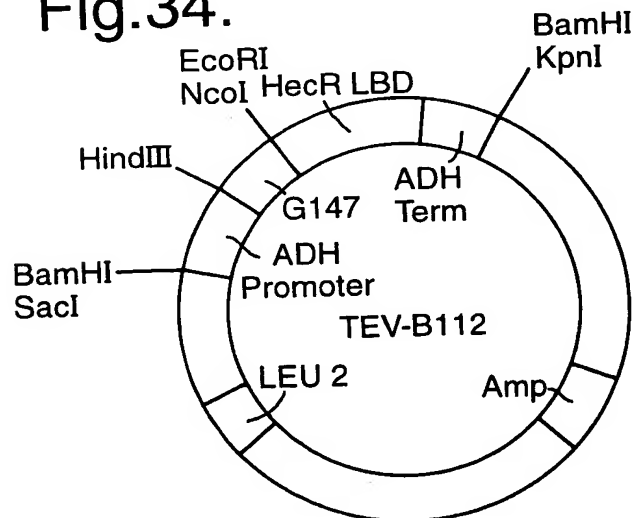


Fig.35.

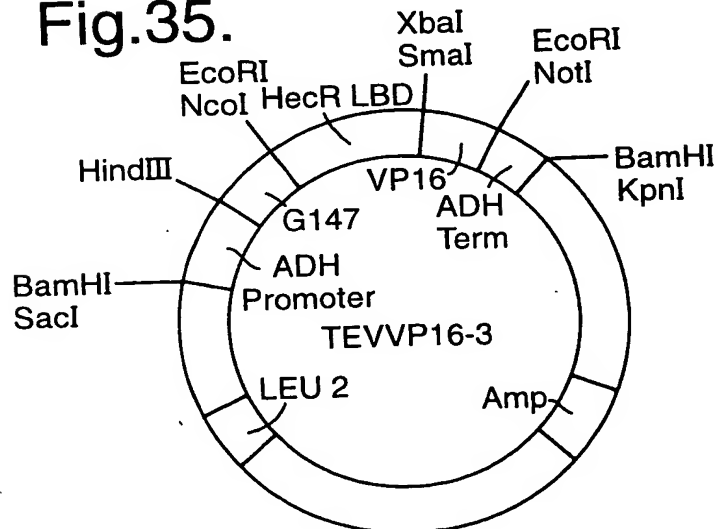


Fig.36.

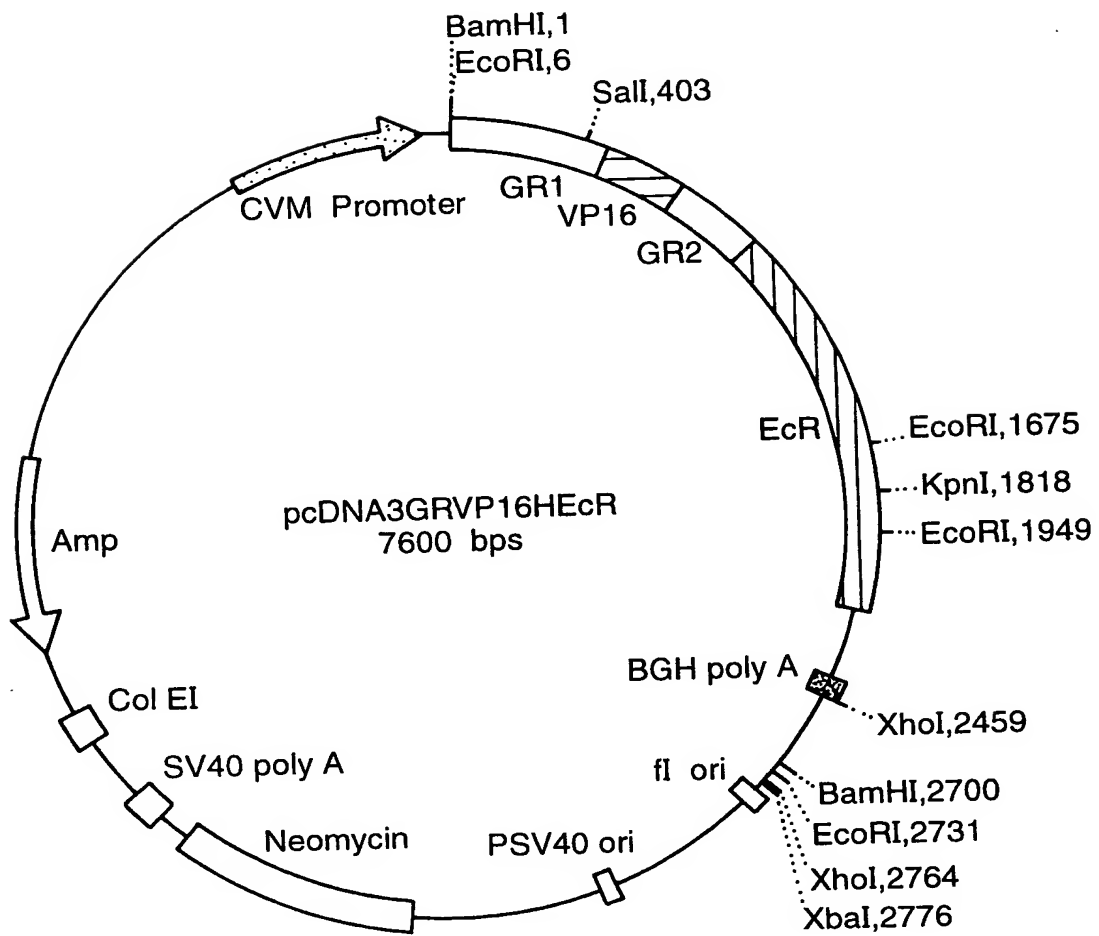




Fig.37.

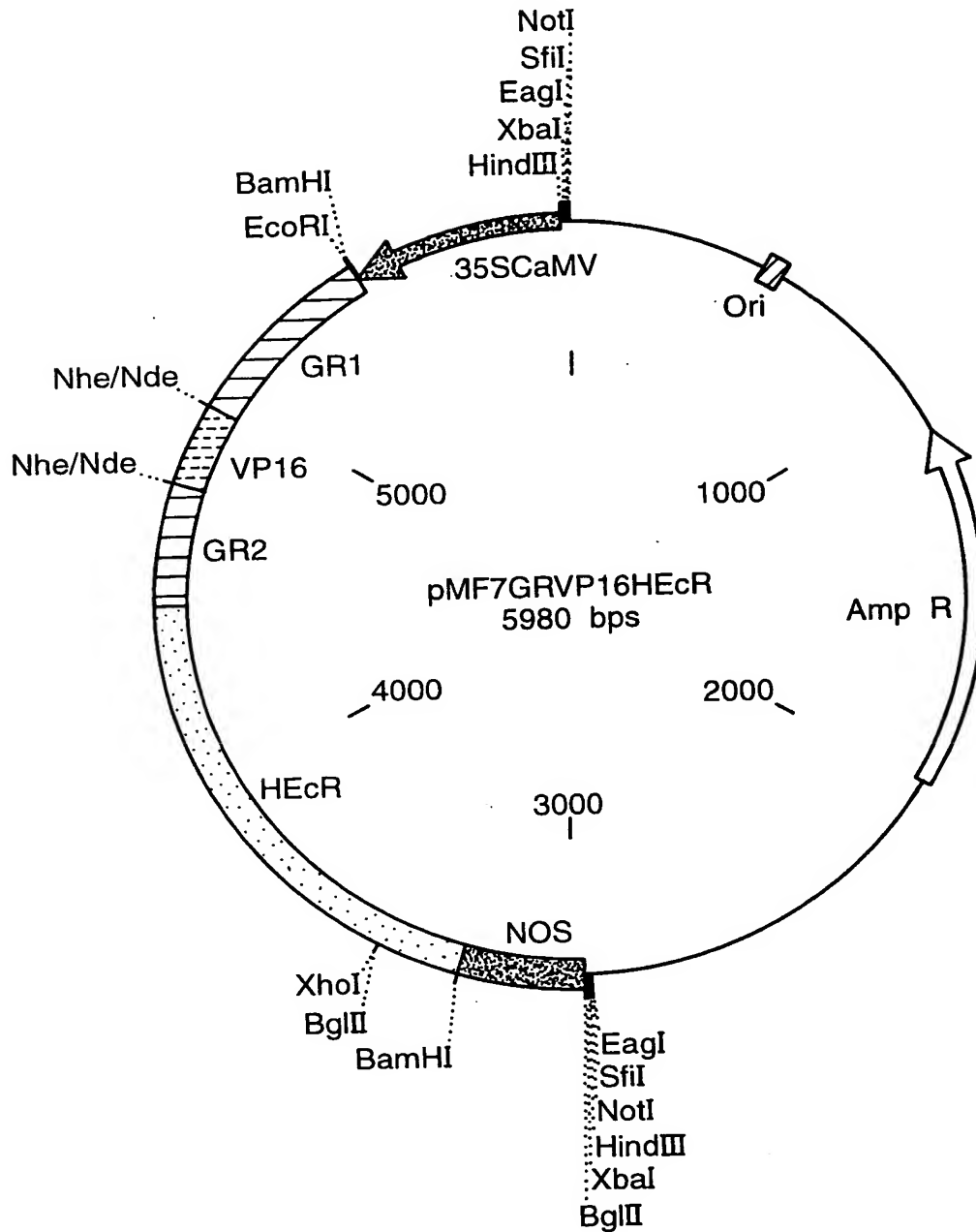


Fig.38.

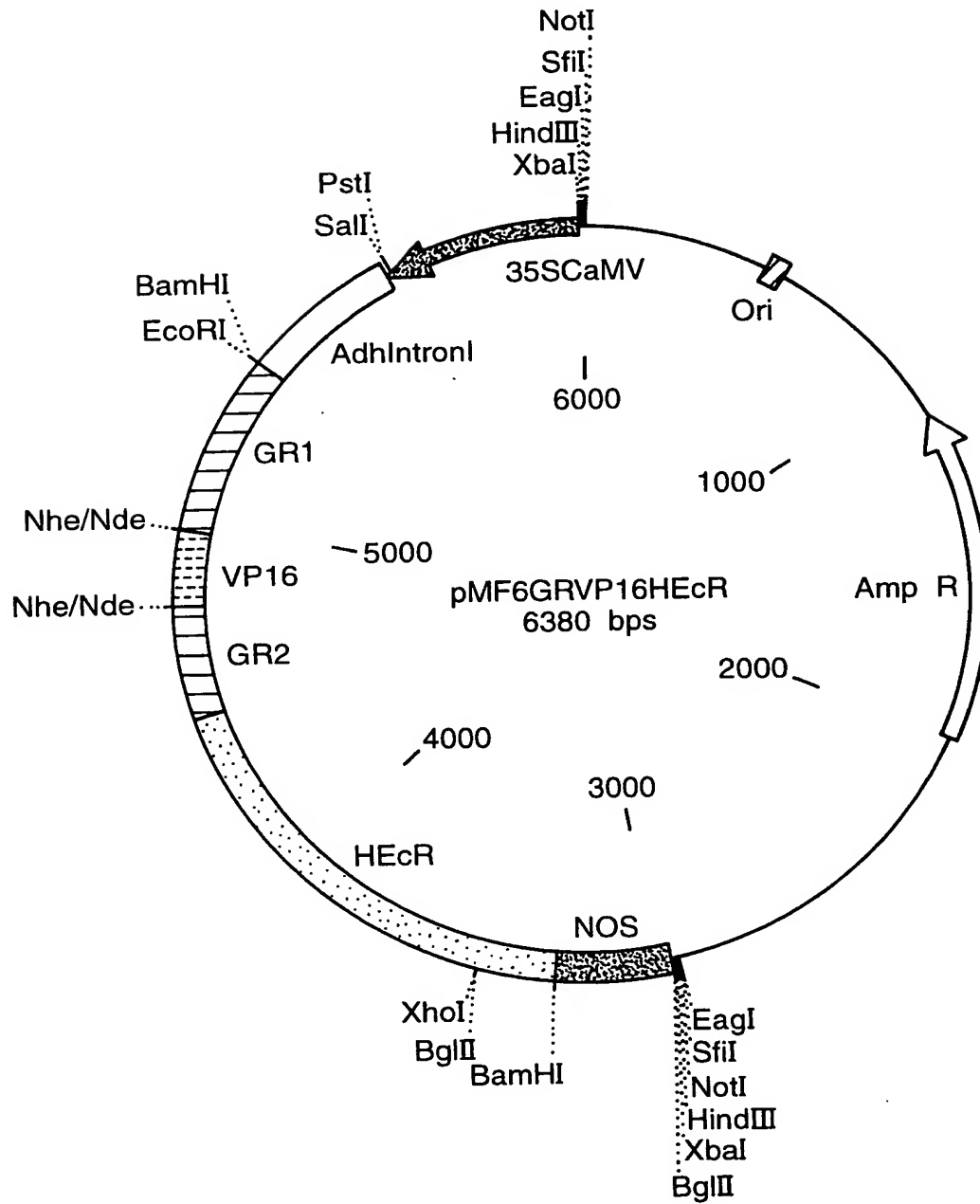
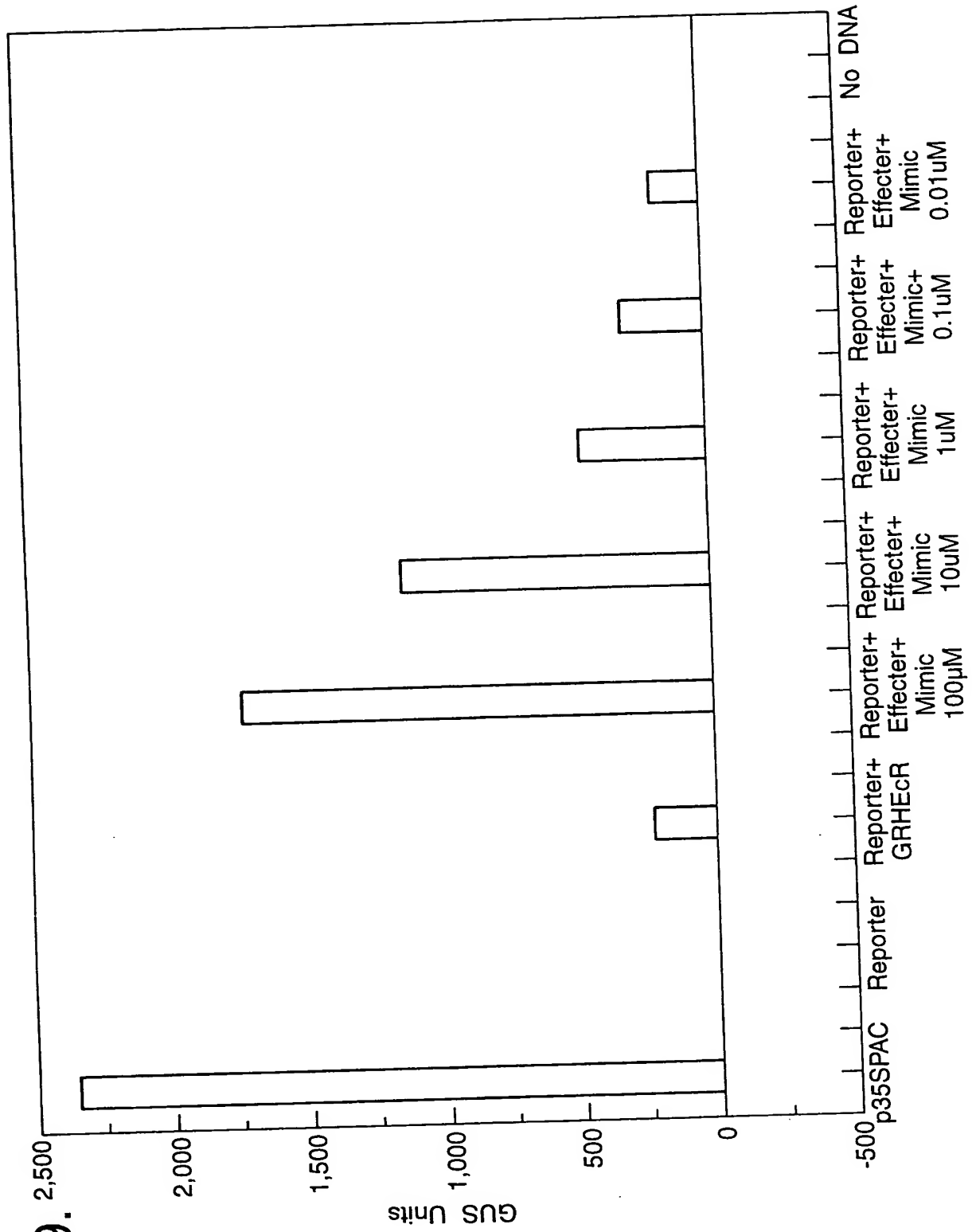


Fig.39.



Spodoptera exigua DNA sequence.

Fig.40.

Sequence ID 6

SPODOPTERA EXIGUA HINGE AND LIGAND BINDING DOMAINS

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 3   | 9   | 15  | 21  | 27  | 33  | 39  | 45  |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 1   | AGG | CCG | GAG | TGC | GTG | CCA | GAA | AAC | CAG | TGT | GCA | ATG | AAA | AGG |     |
|     | TCC | GGC | CTC | ACG | CAC | CAC | GGT | CTT | TTG | GTC | ACA | CGT | TAC | TTT | TCC |
| 46  | AAA | GAG | AAA | AAG | GCA | CAA | AGG | GAA | AAA | GAC | AAG | TTG | CCA | GTC | AGT |
|     | TTT | CTC | TTT | TTC | CGT | GTT | TCC | CTT | TTT | CTG | TTC | AAC | GGT | CAG | TCA |
| 91  | ACA | ACG | ACA | GTG | GAT | GAT | CAC | ATG | CCT | CCC | ATT | ATG | CAG | TGT | GAT |
|     | TGT | TGC | TGT | CAC | CTA | CTA | GTG | TAC | GGA | GGG | TAA | TAC | GTC | ACA | CTA |
| 136 | CCA | CCG | CCT | CCA | GAG | GCC | GCA | AGA | ATT | CAC | GAG | GTG | GTG | CCA | CGA |
|     | GGT | GGC | GGA | GGT | CTC | CGG | CGT | TCT | TAA | GTG | CTC | CAC | CAC | GGT | GCT |
| 181 | TTC | CTG | AAT | GAA | AAG | CTA | ATG | GAC | AGG | ACA | AGG | CTC | AAG | AAT | GTG |
|     | AAG | GAC | TTA | CTT | TTC | GAT | TAC | CTG | TCC | TGT | TCC | GAG | TTC | TTA | CAC |
| 226 | CCC | CCT | CAC | TGC | CAA | CCA | GAA | GTC | CTT | AAT | AGC | GAG | GCT | GGT | CTG |
|     | GGG | GGA | GTG | ACG | GTT | GGT | GGT | CAG | GAA | TTA | TCG | CTC | CGA | CCA | GAC |
| 271 | GTA | CCA | AGA | AGG | CTA | TGA | ACA | GCC | ATC | AGA | AGA | GGA | TCT | AAA | AAG |
|     | CAT | GGT | TCT | TCC | GAT | ACT | TGT | CGG | TAG | TCT | TCT | CCT | AGA | TTT | TTC |

Fig.40 i.

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316 AGT CAC ACA GTC GGA TGA AGA CGA AGA AGA GTC GGA CAT GCC GTT
    TCA GTG TGT CAG CCT ACT TCT GCT TCT TCT CAG CCT GTA CGG CAA

361 CCG TCA GAT CAC CGA GAT GAC GAT CCT CAC AGT GCA GCT CAT TGT
    GGC AGT CTA GTG GCT CTA CTG CTA GGA GTG TCA CGT CGA GTA ACA

406 TGA ATT CGC TAA GGG CCT ACC AGC GTT CGC AAA GAT CTC ACA GTC
    ACT TAA GCG ATT CCC GGA TGG TCG CAA GCG TTT CTA GAG TGT CAG

451 GGA TCA GAT CAC ATT ATT AAA GGC CTG TTC GAG TGA GGT GAT GAT
    CCT AGT CTA GTG TAA TAA TTT CCG GAC AAG CTC ACT CCA CTA CTA

496 GTT GCG AGT AGC TCG GCG GTA CGA CGC GGC GAC AGA CAG CGT GTT
    CAA CGC TCA TCG AGC CGC CAT GCT GCG CCG CTG TCT GTC GCA CAA

541 GTT CGC CAA CAA CCA GGC GTA CAC CCG CGA CAA CTA CCG CAA GGC
    CAA GCG GTT GTT GGT CCG CAT GTG GGC GCT GTT GAT GGC GTT CCG

586 AGG CAT GGC CTA CGT CAT CGA GGA CCT GCT GCA CTT CTG CCG GTG
    TCC GTA CCG GAT GCA GTA GCT CCT GGA CGA CGT GAA GAC GGC CAC

631 CAT GTA CTC CAT GAT GAT GGA TAA CGT CCA CTA TGC ACT GCT CAC
    GTA CAT GAG GTA CTA CTA CCT ATT GCA GGT GAT ACG TGA CGA GTG

676 TGC CAT CGT CAT TTT CTC AGA CCG ACC CGG GCT TGA GCT AAC CCT
    ACG GTA GCA GTA AAA GAG TCT GGC TGG GCC CGA ACT CGA TTG GGA

721 GTT GGT GGA GGA GAT CCA GAG ATA TTA CCT GAA CAC GCT GCG GGT
    CAA CCA CCT CCT CTA GGT CTC TAT AAT GGA CTT GTG CGA CGC CCA

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Fig.40 ii. 766 GTA CAT CCT GAA CCA GAA CAG TCG GTC GCC GTG CTG CCC TGT CAT  
CAT GTA GGA CTT GGT GGC CTT GTC AGC CAG CGG CAC GAC GAG GGG ACA GTA

811 CTA CGC TAA GAT CCT CGG CAT CCT GAC GGA GCT GCG GAC CCT GGG  
GAT GCG ATT CTA GGA GCC GTA GGA CTG CCT CGA CGC CTG GGA CCC

856 CAT GCA GAA CTC CAA CAT GTG CAT CTC ACT CAA GCT GAA GAA CAG  
GTA CGT CTT GAG GTT GTA CAC GTA GAG TGA GTT CGA CTT CTT GTC

901 GAA CGT GCC GCC GTT CTT CGA GGA TAT CTG GGA CGT CCT CGA GTA  
CTT GCA CGG CGG CAA GAA GCT CCT ATA GAC CCT GCA GGA GCT CAT

946 AAA  
TTT

Total number of bases is: 948.

Fig.41.

Sequence I.D. 7

**sequence comparison between Heliothis 19R clone and SecR Taq clone**

|      |   |
|------|---|
| HECR | RPECVVPENQCAMKRKEKKAQREKDKLPVSTTTVDHMPPIMQCDPPPEAARILECVQ                                   |
| SECR | RPECVVPENQCAMKRKEKKAQREKDKLPVSTTTVDHMPPIMQCDPPPEAARI  |
| HECR | HEVVPFRFLNEKLMEQNRLKNVPPLTANQKSLIARLVWYQEGYEQPSEEDLKRVQTQSD                                 |
| SECR | HEVVPFRFLNEKLME <u>TR</u> LRNVPPPLTANQKSLIARLVWYQEGYEQPSEEDLKRVQTQSD                        |
| HECR | EDDESDMPFRQIT <del>EM</del> TILTVQLIVEFAKGLPGFAKISQSDQITLLKACSS <del>EV</del> MMLR          |
| SECR | EDEESDMPFRQIT <del>EM</del> TILTVQLIVEFAKGLP <u>AF</u> AKISQSDQITLLKACSS <del>EV</del> MMLR |
| HECR | VARRYDAATDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMMMDNVHYALL                                   |
| SECR | VARRYDAATDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMMMDNVHYALL                                   |
| HECR | TAIVIFSDRPGLEQPLLVEEIQRYLNTLRVYILNQNSASPRGAVIFGEILGILTEI                                    |
| SECR | TAIVIFSDRPGLE <u>L</u> TLLVEEIQRYLNTLRVYILNQNSRSPCCPVIYAK <u>IL</u> GILTEL                  |
| HECR | RTLGMQNSNMCISLKLKKRKLPPFLEEIDWDV  |
| SECR | RTLGMQNSNMCISLKLKNRNVPPFF <u>E</u> DIDWDV   |

Fig.42.

